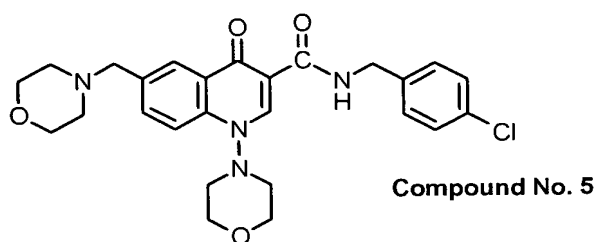
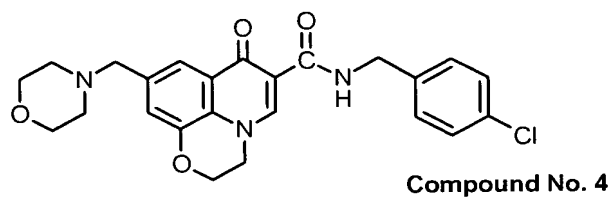
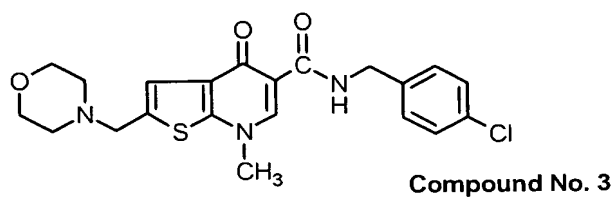
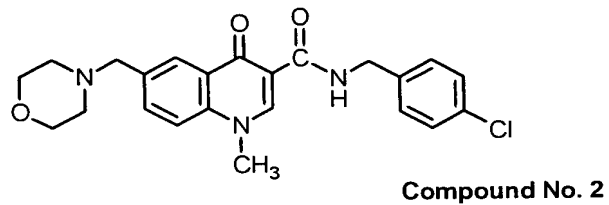
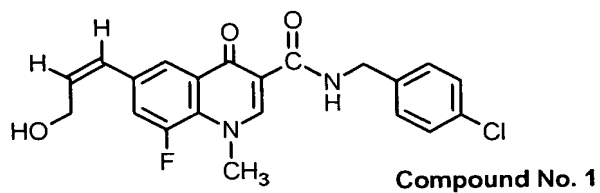
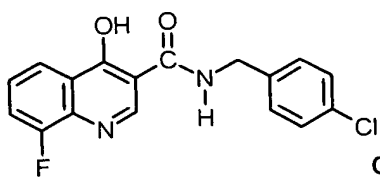
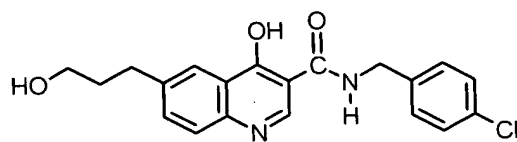


Figure 1 **4-HQ, 4-oxo-DHQ and 4-oxo-DHTP antiviral compounds**

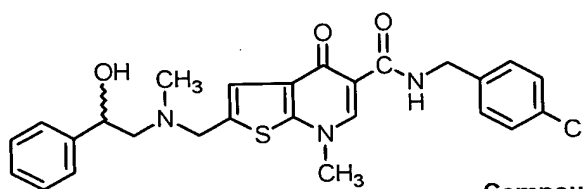
(Figure 1 continue)



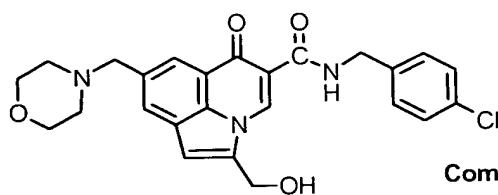
Compound No. 6



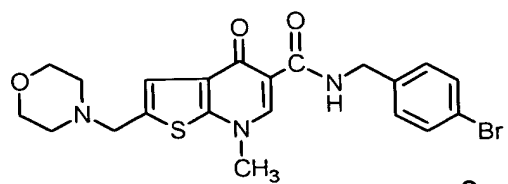
Compound No. 7



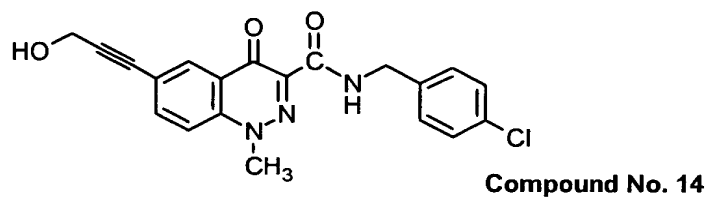
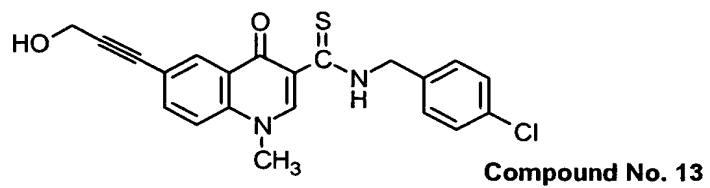
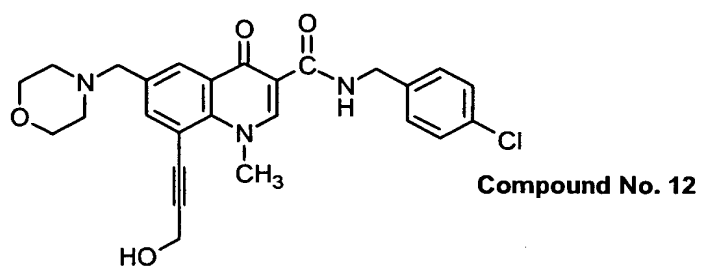
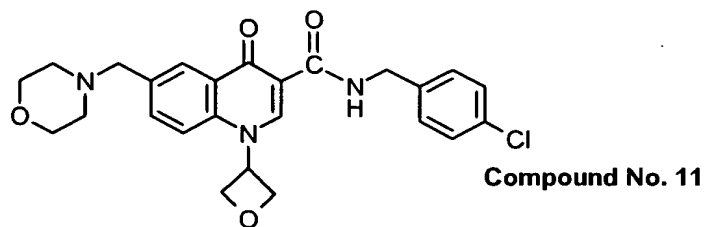
Compound No. 8



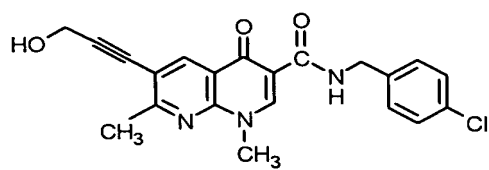
Compound No. 9



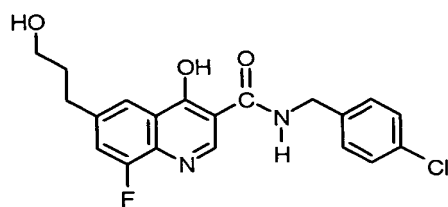
Compound No. 10

(Figure 1 continue)

(Figure 1 continue)

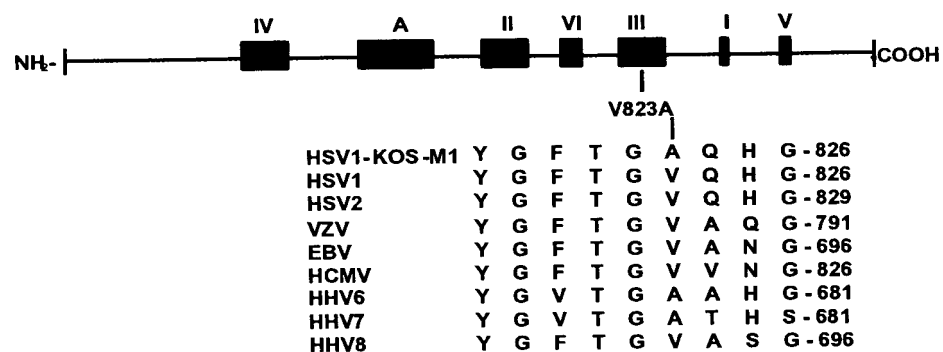


Compound No.15



Compound 17

Figure 2. The HSV1 (KOS Strain) DNA Polymerase Amino Acid 823 is Critical for Resistance to 4-Hydroxyquinolines and Related Compounds



Schematic of HSV1 polymerase illustrating the conserved regions A and I-VI found in class 2 polymerases. Also shown are the amino acid sequence for the highly conserved herpesvirus domain in region III which surrounds the HSV1 amino acid 823.

Figure 3 **Serial Passage of HSV-1 in Presence of 20 μ M compound 17**

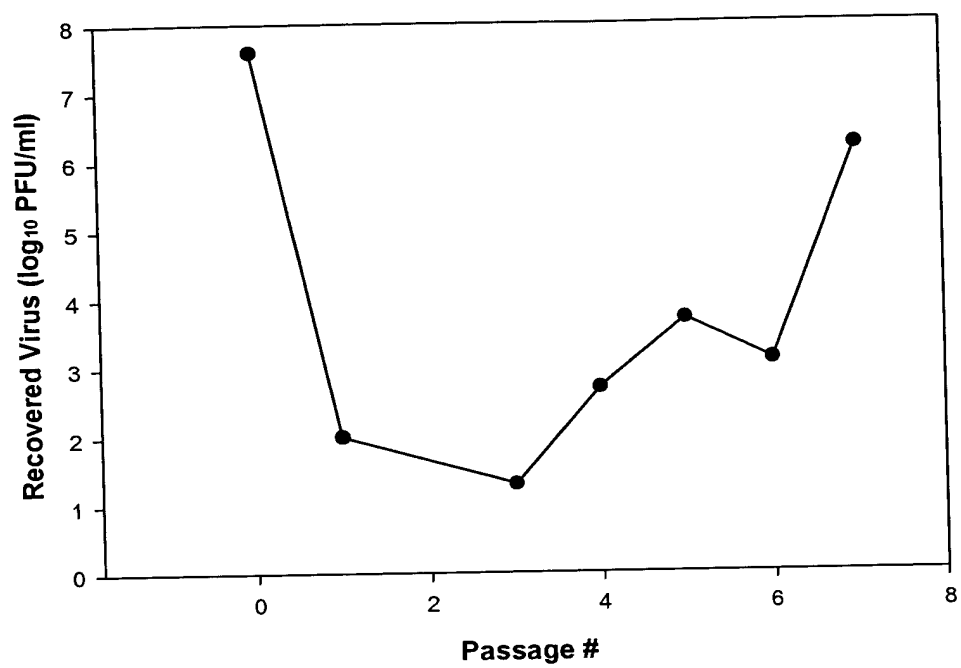


Figure 4 Comparison of Wild type HSV-1 and HSV-2 DNA Polymerases Amino Acid Sequences Aligned by Amino Acid Homology*

| | | | | | | | |
|----|-------------|------------|------------|------------|------------|------------|------|
| 5 | HSV2-MS | MFCAAGGPTS | PGGKSAARAA | SGFFAPHNPR | GATQTAPPPC | RRQNFYNPHL | -50 |
| | HSV2-186 | MFCAAGGPAS | PGGKSAARAA | SGFFAPHNPR | GATQTAPPPC | RRQNFYNPHL | -50 |
| | HSV1-Kos | MFSGGGGPLS | PGGKSAARAA | SGFFAPAGPR | GAGR.GPPPC | LRQNFYNPYL | -49 |
| | HSV1-Patton | MFSGGGGPLS | PGGKSAARAA | SGFFAPAGPR | GAGR.GPPPC | LRQNFYNPYL | -49 |
| | HSV1-DJL | MFSGGGGPLS | PGGKSAARAA | SGFFAPAGPR | GAGR.GPPPC | LRQNFYNPYL | -49 |
| | HSV1-F | MFSGGGGPLS | PGGKSAARAA | SGFFAPAGPR | GAGR.GPPPC | LRQNFYNPYL | -49 |
| 10 | HSV2-MS | AQTGTQPKAP | GPAQRHTYYS | ECDEFRLFAP | RSLDEDAPAE | QRTGVHDGRL | -100 |
| | HSV2-186 | AQTGTQPKAP | GPAQRHTYYS | ECDEFRLFAP | RSLDEDAPAE | QRTGVHDGRL | -100 |
| | HSV1-Kos | APVGTQQKPT | GPTQRHTYYS | ECDEFRLFAP | RVLDEDAPPE | KRAGVHDGHL | -99 |
| | HSV1-Patton | APVGTQQKPT | GPTQRHTYYS | ECDEFRLFAP | RVLDEDAPPE | KRAGVHDGHL | -99 |
| | HSV1-DJL | APVGTQQKPT | GPTQRHTYYS | ECDEFRLFAP | RVLDEDAPPE | KRAGVHDGHL | -99 |
| | HSV1-F | APVGTQQKPT | GPTQRHTYYS | ECDEFRLFAP | RVLDEDAPPE | KRAGVHDGHL | -99 |
| 20 | HSV2-MS | RRAPKVYCGG | DERDVLRVGP | EGFWPRRLRL | WGGADHAPKG | FDPTVTVFHV | -150 |
| | HSV2-186 | RRAPKVYCGG | DERDVLRVGP | EGFWPRRLRL | WGGADHAPKG | FDPTVTVFHV | -150 |
| | HSV-Kos | KRAPKVYCGG | DERDVLRVGS | GGFWPRRSRL | WGGVDHAPAG | FNPTVTVFHV | -149 |
| | HSV1-Patton | KRAPKVYCGG | DERDVLRVGS | GGFWPRRSRL | WGGVDHAPAG | FNPTVTVFHV | -149 |
| | HSV1-DJL | KRAPKVYCGG | DERDVLRVGS | GGFWPRRSRL | WGGVDHAPAG | FNPTVTVFHV | -149 |
| | HSV1-F | KRAPKVYCGG | DERDVLRVGS | GGFWPRRSRL | WGGVDHAPAG | FNPTVTVFHV | -149 |
| 25 | HSV2-MS | YDILEHVEHA | YSMRAAQLHE | RFMDAITPAG | TVITLLGLTP | EGHRVAVHVV | -200 |
| | HSV2-186 | YDILEHVEHA | YSMRAAQLHE | RFMDAITPAG | TVITLLGLTP | EGHRVAVHVV | -200 |
| | HSV-Kos | YDILENVEHA | YGMRAAQFHA | RFMDAITPTG | TVITLLGLTP | EGHRVAVHVV | -199 |
| | HSV1-Patton | YDILENVEHA | YGMRAAQFHA | RFMDAITPTG | TVITLLGLTP | EGHRVAVHVV | -199 |
| | HSV1-DJL | YDILENVEHA | YGMRAAQFHA | RFMDAITPTG | TVITLLGLTP | EGHRVAVHVV | -199 |
| | HSV1-F | YDILENVEHA | YGMRAAQFHA | RFMDAITPTG | TVITLLGLTP | EGHRVAVHVV | -199 |
| 30 | HSV2-MS | GTRQYFYMNK | AEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -250 |
| | HSV2-186 | GTRQYFYMNK | AEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -250 |
| | HSV-Kos | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| | HSV1-Patton | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| | HSV1-DJL | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| | HSV1-F | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| 35 | HSV2-MS | GTRQYFYMNK | AEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -250 |
| | HSV2-186 | GTRQYFYMNK | AEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -250 |
| | HSV-Kos | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| | HSV1-Patton | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| | HSV1-DJL | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| | HSV1-F | GTRQYFYMNK | EEVDRHLQCR | APRDLCECLA | AALRESPGAS | FRGISADHFE | -249 |
| 40 | HSV2-MS | AEVVERADV | YYETRPTLYY | RVFVRSGRAL | AYLCDNFCPA | IRKYEGGVDA | -300 |
| | HSV2-186 | AEVVERADV | YYETRPTLYY | RVFVRSGRAL | AYLCDNFCPA | IRKYEGGVDA | -300 |
| | HSV-Kos | AEVVERTDVY | YYETRPALFY | RVYVRSGRVL | SYLCDNFCPA | IKKYEGGVDA | -299 |
| | HSV1-Patton | AEVVERTDVY | YYETRPALFY | RVYVRSGRVL | SYLCDNFCPA | IKKYEGGVDA | -299 |
| | HSV1-DJL | AEVVERTDVY | YYETRPALFY | RVYVRSGRVL | SYLCDNFCPA | IKKYEGGVDA | -299 |
| | HSV1-F | AEVVERTDVY | YYETRPALFY | RVYVRSGRVL | SYLCDNFCPA | IKKYEGGVDA | -299 |
| 45 | HSV2-MS | TTRFILDNPG | FVTFGWYRLK | PGRGNAPAQ | RPPTAFGTSS | DVEFNCTADN | -350 |
| | HSV2-186 | TTRFILDNPG | FVTFGWYRLK | PGRGNAPAQ | RPPTAFGTSS | DVEFNCTADN | -350 |
| | HSV-Kos | TTRFILDNPG | FVTFGWYRLK | PGRNNTLAQ | RAPMAFGTSS | DVEFNCTADN | -349 |
| | HSV1-Patton | TTRFILDNPG | FVTFGWYRLK | PGRNNTLAQ | RAPMAFGTSS | DVEFNCTADN | -349 |
| | HSV1-DJL | TTRFILDNPG | FVTFGWYRLK | PGRNNTLAQ | RAPMAFGTSS | DVEFNCTADN | -349 |
| | HSV1-F | TTRFILDNPG | FVTFGWYRLK | PGRNNTLAQ | RAPMAFGTSS | DVEFNCTADN | -349 |
| 50 | HSV2-MS | LAVEGAMCDL | PAYKLMCFDI | ECKAGGEDEL | AFPVAERPED | LVIQISCLLY | -400 |
| | HSV2-186 | LAVEGAMCDL | PAYKLMCFDI | ECKAGGEDEL | AFPVAERPED | LVIQISCLLY | -400 |
| | HSV-Kos | LAIEGGMSDL | PAYKLMCFDI | ECKAGGEDEL | AFPVAGHPED | LVIQISCLLY | -399 |
| | HSV1-Patton | LAIEGGMSDL | PAYKLMCFDI | ECKAGGEDEL | AFPVAGHPED | LVIQISCLLY | -399 |
| | HSV1-DJL | LAIEGGMSDL | PAYKLMCFDI | ECKAGGEDEL | AFPVAGHPED | LVIQISCLLY | -399 |
| | HSV1-F | LAIEGGMSDL | PAYKLMCFDI | ECKAGGEDEL | AFPVAGHPED | LVIQISCLLY | -399 |
| 55 | HSV2-MS | DLSTTALEHI | LLFSLGSCDL | PESHLSDLAS | RGLPAPVVLE | FDSEFEMLLA | -450 |
| | HSV2-186 | DLSTTALEHI | LLFSLGSCDL | PESHLSDLAS | RGLPAPVVLE | FDSEFEMLLA | -450 |
| | HSV-Kos | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| | HSV1-Patton | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| | HSV1-DJL | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| | HSV1-F | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| 60 | HSV2-MS | DLSTTALEHI | LLFSLGSCDL | PESHLSDLAS | RGLPAPVVLE | FDSEFEMLLA | -450 |
| | HSV2-186 | DLSTTALEHI | LLFSLGSCDL | PESHLSDLAS | RGLPAPVVLE | FDSEFEMLLA | -450 |
| | HSV-Kos | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| | HSV1-Patton | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| | HSV1-DJL | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |
| | HSV1-F | DLSTTALEHV | LLFSLGSCDL | PESHLNELAA | RGLPTPVVLE | FDSEFEMLLA | -449 |

| | | | | | | | |
|----|-------------|------------|------------|------------|------------|------------|------|
| 5 | HSV2-MS | FMTFVKQYGP | EFVTGYNIIN | FDWPFVLTCL | TEIYKVPLDG | YGRMNNGRVF | -500 |
| | HSV2-186 | FMTFVKQYGP | EFVTGYNIIN | FDWPFVLTCL | TEIYKVPLDG | YGRMNNGRVF | -500 |
| | HSV-Kos | FMTLVKQYGP | EFVTGYNIIN | FDWPFLLAKL | TDIYKVPLDG | YGRMNNGRVF | -499 |
| | HSV1-Patton | FMTLVKQYGP | EFVTGYNIIN | FDWPFLLAKL | TDIYKVPLDG | YGRMNNGRVF | -499 |
| | HSV1-DJL | FMTLVKQYGP | EFVTGYNIIN | FDWPFLLAKL | TDIYKVPLDG | YGRMNNGRVF | -499 |
| | HSV1-F | FMTLVKQYGP | EFVTGYNIIN | FDWPFLLAKL | TDIYKVPLDG | YGRMNNGRVF | -499 |
| 10 | HSV2-MS | RVWDIGQSHF | QKRSKIKVNG | MVNIDMYGII | TDKVKLSSYK | LNAVAEAVLK | -550 |
| | HSV2-186 | RVWDIGQSHF | QKRSKIKVNG | MVNIDMYGII | TDKVKLSSYK | LNAVAEAVLK | -550 |
| | HSV-Kos | RVWDIGQSHF | QKRSKIKVNG | MVNIDMYGII | TDKIKLSSYK | LNAVAEAVLK | -549 |
| | HSV1-Patton | RVWDIGQSHF | QKRSKIKVNG | MVNIDMYGII | TDKIKLSSYK | LNAVAEAVLK | -549 |
| | HSV1-DJL | RVWDIGQSHF | QKRSKIKVNG | MVNIDMYGII | TDKIKLSSYK | LNAVAEAVLK | -549 |
| | HSV1-F | RVWDIGQSHF | QKRSKIKVNG | MVNIDMYGII | TDKIKLSSYK | LNAVAEAVLK | -549 |
| 15 | HSV2-MS | DKKKDLSDYR | IPAYYASGPA | QRGVIGEYCV | QDSLLVGQLF | FKFLPHLELS | -600 |
| | HSV2-186 | DKKKDLSDYR | IPAYYASGPA | QRGVIGEYCV | QDSLLVGQLF | FKFLPHLELS | -600 |
| | HSV-Kos | DKKKDLSDYR | IPAYYAAGPA | QRGVIGEYCI | QDSLLVGQLF | FKFLPHLELS | -599 |
| | HSV1-Patton | DKKKDLSDYR | IPAYYAAGPA | QRGVIGEYCI | QDSLLVGQLF | FKFLPHLELS | -599 |
| | HSV1-DJL | DKKKDLSDYR | IPAYYAAGPA | QRGVIGEYCI | QDSLLVGQLF | FKFLPHLELS | -599 |
| | HSV1-F | DKKKDLSDYR | IPAYYAAGPA | QRGVIGEYCI | QDSLLVGQLF | FKFLPHLELS | -599 |
| 25 | HSV2-MS | AVARLAGINI | TRTIYDGQQI | RVFTCLLRLL | GQKGFILPDT | QGRFRGLDKE | -650 |
| | HSV2-186 | AVARLAGINI | TRTIYDGQQI | RVFTCLLRLL | GQKGFILPDT | QGRFRGLDKE | -650 |
| | HSV-Kos | AVARLAGINI | TRTIYDGQQI | RVFTCLLRLL | DQKGFILPDT | QGRFRGAGGE | -649 |
| | HSV1-Patton | AVARLAGINI | TRTIYDGQQI | RVFTCLLRLL | DQKGFILPDT | QGRFRGAGGE | -649 |
| | HSV1-DJL | AVARLAGINI | TRTIYDGQQI | RVFTCLLRLL | DQKGFILPDT | QGRFRGAGGE | -649 |
| | HSV1-F | AVARLAGINI | TRTIYDGQQI | RVFTCLLRLL | DQKGFILPDT | QGRFRGGGGE | -649 |
| 30 | HSV2-MS | APKRPAVPRG | EGERP GDNG | DEKDDDE.. | DEGDERE.E | VARETGGRHV | -697 |
| | HSV2-186 | APKRPAVPRG | EGERP GDNG | DEKDDDEDEG | DEGDERE.E | VARETGGRHV | -697 |
| | HSV-Kos | APKRPAARE | DEERP..... | EEGEDEDER | EEGGGEREPE | GARETAGRHV | -694 |
| | HSV1-Patton | APKRPAARE | DEERP..... | EEGEDEDER | EEGGGEREPE | GARETAGRHV | -694 |
| | HSV1-DJL | APKRPAARE | DEERP..... | EEGEDENER | EEGGGEREPE | GARETAGRHV | -694 |
| | HSV1-F | APKRPAARE | DEERP..... | EEGEDEDER | EEGGGEREPE | GARETAGRHV | -694 |
| 40 | HSV2-MS | GYQGARVLDP | TSGFHVDPVV | VDFASLYPS | IIQAHNLCFS | TLSLRPEAVA | -747 |
| | HSV2-186 | GYQGARVLDP | TSGFHVDPVV | VDFASLYPS | IIQAHNLCFS | TLSLRPEAVA | -749 |
| | HSV-Kos | GYQGARVLDP | TSGFHVNPVV | VDFASLYPS | IIQAHNLCFS | TLSLRADAVA | -744 |
| | HSV1-Patton | GYQGARVLDP | ISGFHVNPVV | VDFASLYPS | IIQAHNLCFS | TLSLRADAVA | -744 |
| | HSV1-DJL | GYQGARVLDP | TSGFHVNPVV | VDFASLYPS | IIQAHNLCFS | TLSLRADAVA | -744 |
| | HSV1-F | GYQGARVLDP | TSGFHVNPVV | VDFASLYPS | IIQAHNLCFS | TLSLRADAVA | -744 |
| 45 | HSV2-MS | HLEARDYLE | IEVGRRRLFF | VKAHVRESLL | SILLRDWLAM | RKQIRSRIPQ | -797 |
| | HSV2-186 | HLEARDYLE | IEVGRRRLFF | VKAHVRESLL | SILLRDWLAM | RKQIRSRIPQ | -799 |
| | HSV-Kos | HLEAGDYLE | IEVGRRRLFF | VKAHVRESLL | SILLRDWLAM | RKQIRSRIPQ | -794 |
| | HSV1-Patton | HLEAGDYLE | IEVGRRRLFF | VKAHVRESLL | SILLRDWLAM | RKQIRSRIPQ | -794 |
| | HSV1-DJL | HLEAGDYLE | IEVGRRRLFF | VKAHVRESLL | SILLRDWLAM | RKQIRSRIPQ | -794 |
| | HSV1-F | HLEAGDYLE | IEVGRRRLFF | VKAHVRESLL | SILLRDWLAM | RKQIRSRIPQ | -794 |
| 50 | HSV2-MS | STPEEAVLLD | KQQAIAKVV | NSVYGFTGVQ | HGLLPCLHVA | ATVTTIGREM | -847 |
| | HSV2-186 | STPEEAVLLD | KQQAIAKVV | NSVYGFTGVQ | HGLLPCLHVA | ATVTTIGREM | -849 |
| | HSV-Kos | SSPEEAVLLD | KQQAIAKVV | NSVYGFTGVQ | HGLLPCLHVA | ATVTTIGREM | -844 |
| | HSV1-Patton | SSPEEAVLLD | KQQAIAKVV | NSVYGFTGVQ | HGLLPCLHVA | ATVTTIGREM | -844 |
| | HSV1-DJL | SSPEEAVLLD | KQQAIAKVV | NSVYGFTGVQ | HGLLPCLHVA | ATVTTIGREM | -844 |
| | HSV1-F | SSPEEAVLLD | KQQAIAKVV | NSVYGFTGVQ | HGLLPCLHVA | ATVTTIGREM | -844 |
| 60 | HSV2-MS | LLATRAYVHA | RWAEFDQLLA | DFPEAAGMRA | PGPYSMRIIY | GDTDSIFVLC | -897 |
| | HSV2-186 | LLATRAYVHA | RWAEFDQLLA | DFPEAAGMRA | PGPYSMRIIY | GDTDSIFVLC | -899 |
| | HSV-Kos | LLATREYVHA | RWAAFEQLLA | DFPEADMRA | PGPYSMRIIY | GDTDSIFVLC | -894 |
| | HSV1-Patton | LLATREYVHA | RWAAFEQLLA | DFPEADMRA | PGPYSMRIIY | GDTDSIFVLC | -894 |
| | HSV1-DJL | LLATREYVHA | RWAAFEQLLA | DFPEADMRA | PGPYSMRIIY | GDTDSIFVLC | -894 |
| | HSV1-F | LLATREYVHA | RWAAFEQLLA | DFPEADMRA | PGPYSMRIIY | GDTDSIFVLC | -894 |
| 65 | HSV2-MS | RGLTAAGLVA | MGDKMASHIS | RALFLPPIKL | ECEKTFTKLL | LIAKKKYIGV | -947 |

| | | | | | | | |
|----|-------------|------------|------------|------------|------------|-------------|-------|
| | HSV2-186 | RGLTAAGLVA | MGDKMASHIS | RALFLPPIKL | ECEKTFTKLL | LIAKKKYIGV | -949 |
| | HSV-Kos | RGLTAAGLTA | MGDKMASHIS | RALFLPPIKL | ECEKTFTKLL | LIAKKKYIGV | -944 |
| | HSV1-Patton | RGLTAAGLTA | MGDKMASHIS | RALFLPPIKL | ECEKTFTKLL | LIAKKKYIGV | -944 |
| | HSV1-DJL | RGLTAAGLTA | VGDKMASHIS | RALFLPPIKL | ECEKTFTKLL | LIAKKKYIGV | -944 |
| 5 | HSV1-F | RGLTAAGLTA | VGDKMASHIS | RALFLSPIKL | ECEKTFTKLL | LIAKKKYIGV | -944 |
| | HSV2-MS | ICGGKMLIKG | VDLVRKNNCA | FINRTSRALV | DLLFYDDTVS | GAAAAALAERP | -997 |
| | HSV2-186 | ICGGKMLIKG | VDLVRKNNCA | FINRTSRALV | DLLFYDDTVS | GAAAAALAERP | -999 |
| | HSV-Kos | IYGGKMLIKG | VDLVRKNNCA | FINRTSRALV | DLLFYDDTVS | GAAAAALAERP | -994 |
| 10 | HSV1-Patton | IYGGKMLIKG | VDLVRKNNCA | FINRTSRALV | DLLFYDDTVS | GAAAAALAERP | -994 |
| | HSV1-DJL | IYGGKMLIKG | VDLVRKNNCA | FINRTSRALV | DLLFYDDTVS | GAAAAALAERP | -994 |
| | HSV1-F | IYGGKMLIKG | VDLVRKNNCA | FINRTSRALV | DLLFYDDTVS | GAAAAALAERP | -994 |
| | HSV2-MS | AEEWLARPLP | EGLQAFGAVL | VDAHRRITDP | ERDIQDFVLT | AELSRHPRAY | -1047 |
| 15 | HSV2-186 | AEEWLARPLP | EGLQAFGAVL | VDAHRRITDP | ERDIQDFVLT | AELSRHPRAY | -1049 |
| | HSV-Kos | AEEWLARPLP | EGLQAFGAVL | VDAHRRITDP | ERDIQDFVLT | AELSRHPRAY | -1044 |
| | HSV1-Patton | AEEWLARPLP | EGLQAFGAVL | VDAHRRITDP | ERDIQDFVLT | AELSRHPRAY | -1044 |
| | HSV1-DJL | AEEWLARPLP | EGLQAFGAVL | VDAHRRITDP | ERDIQDFVLT | AELSRHPRAY | -1044 |
| | HSV1-F | AEEWLARPLP | EGLQAFGAVL | VDAHRRITDP | ERDIQDFVLT | AELSRHPRAY | -1044 |
| 20 | HSV2-MS | TNKRLAHLTV | YYKLMARRAQ | VPSIKDRIPY | VIVAQTREVE | ETVARLAALR | -1097 |
| | HSV2-186 | TNKRLAHLTV | YYKLMARRAQ | VPSIKDRIPY | VIVAQTREVE | ETVARLAALR | -1099 |
| | HSV-Kos | TNKRLAHLTV | YYKLMARRAQ | VPSIKDRIPY | VIVAQTREVE | ETVARLAALR | -1094 |
| | HSV1-Patton | TNKRLAHLTV | YYKLMARRAQ | VPSIKDRIPY | VIVAQTREVE | ETVARLAALR | -1094 |
| 25 | HSV1-DJL | TNKRLAHLTV | YYKLMARRAQ | VPSIKDRIPY | VIVAQTREVE | ETVARLAALR | -1094 |
| | HSV1-F | TNKRLAHLTV | YYKLMARRAQ | VPSIKDRIPY | VIVAQTREVE | ETVARLAALR | -1094 |
| | HSV2-MS | ELDAAAPGDE | PAPPAALPSP | AKRPRETPSH | ADPPGGASKP | RKLLVSELAE | -1147 |
| | HSV2-186 | ELDAAAPGDE | PAPPAALPSP | AKRPRETPSH | ADPPGGASKP | RKLLVSELAE | -1149 |
| 30 | HSV-Kos | ELDAAAPGDE | PAPPAALPSP | AKRPRETPSH | ADPPGGASKP | RKLLVSELAE | -1144 |
| | HSV1-Patton | ELDAAAPGDE | PAPPAALPSP | AKRPRETPSP | ADPPGGASKP | RKLLVSELAE | -1144 |
| | HSV1-DJL | ELDAAAPGDE | PAPPAALPSP | AKRPRETPSP | ADPPGGASKP | RKLLVSELAE | -1144 |
| | HSV1-F | ELDAAAPGDE | PAPPAALPSP | AKRPRETPLH | ADPPGGASKP | RKLLVSELAE | -1144 |
| 35 | HSV2-MS | DPGYAIARGV | PLNTDYYFSH | LLGAACVTFK | ALFGNNAKIT | ESLLKRFIPE | -1197 |
| | HSV2-186 | DPGYAIARGV | PLNTDYYFSH | LLGAACVTFK | ALFGNNAKIT | ESLLKRFIPE | -1199 |
| | HSV-Kos | DPAYAIAHGV | ALNTDYYFSH | LLGAACVTFK | ALFGNNAKIT | ESLLKRFIPE | -1194 |
| | HSV1-Patton | DPAYAIAHGV | ALNTDYYFSH | LLGAACVTFK | ALFGNNAKIT | ESLLKRFIPE | -1194 |
| | HSV1-DJL | DPAYAIAHGV | ALNTDYYFSH | LLGAACVTFK | ALFGNNAKIT | ESLLKRFIPE | -1194 |
| 40 | HSV1-F | DPAYAIAHGV | ALNTDYYFSH | LLGAACVTFK | ALFGNNAKIT | ESLLKRFIPE | -1194 |
| | HSV2-MS | TWHPPDDVAA | RLRAAGFGPA | GAGATAEETR | RMLHRAFDTL | A* -1238 | |
| | HSV2-186 | TWHPPDDVAA | RLRAAGFGPA | GAGATAEETR | RMLHRAFDTL | A* -1240 | |
| | HSV-Kos | VWHPPDDVAA | RLRAAGFGAV | GAGATAEETR | RMLHRAFDTL | A* -1235 | |
| 45 | HSV1-Patton | VWHPPDDVTA | RLRAAGFGAV | GAGATAEETR | RMLHRAFDTL | A* -1235 | |
| | HSV1-DJL | VWHPPDDVAA | RLRTAGFGAV | GAGATAEETR | RMLHRAFDTL | A* -1235 | |
| | HSV1-F | VWHPPDDVAA | RLRAAGFGAV | GAGATAEETR | RMLHRAFDTL | A* -1235 | |

*Amino acid alignment demonstrates difference in amino acid's sequences.

50 *The gaps "....." indicate missing amino acids relative to other stanins.

*Wild HSV2-MS is listed as SEQ. ID NO 14.

*Wild HSV2-186 is listed as SEQ. ID NO 15.

*Wild HSV-Kos is listed as SEQ. ID NO 16.

*Wild HSV1-Patton is listed as SEQ. ID NO 17.

55 *Wild HSV1-DJL is listed as SEQ. ID NO 18.

*Wild HSV1-F is listed as SEQ. ID NO 19.

Figure 5 DNA and amino acid sequence list**SEQ. ID. NO. 1** DNA sequence of DNA polymerase gene for HSV2-MS-M1

5 1 ATGTTTTGTG CCGCGGGCGG CCCGACTTCC CCCGGGGGGA AGTCGGCGGC
 51 TCGGGCGGCG TCTGGGTTTT TTGCCCCCA CAACCCCGG GGAGCCACCC
 10 101 AGACGGCACC GCCGCCTTGC CGCCGGCAGA ACTTCTACAA CCCCACCTC
 151 GCTCAGACCG GAACGCAGCC AAAGGCCCCC GGGCCGGCTC AGCGCCATAC
 201 GTACTACAGC GAGTGCACG AATTTCGATT TATCGCCCCG CGTTCGCTGG
 15 251 ACGAGGACGC CCCC GCGGAG CAGCGCACCG GGGTCCACGA CGGCCGCCTC
 301 CGGCGCGCCC CTAAGGTGTA CTGCGGGGGG GACGAGCGCG ACGTCCTCCG
 20 351 CGTGGGCCCC GAGGGCTTCT GGCCGCGTCG CTTGCGCCTG TGGGGCGGTG
 401 CGGACCATGC CCCCAAGGGG TTCGACCCA CCGTCACCGT CTTCCACGTG
 451 TACGACATCC TGGAGCACGT GGAACACGCG TACAGCATGC GCGCCGCCCA
 25 501 GCTCCACGAG CGATTTATGG ACGCCATCAC GCCCGCCGGG ACCGTCATCA
 551 CGCTTCTGGG TCTGACCCCC GAAGGCCATC GCGTCGCCGT TCACGTCTAC
 30 601 GGCACGCGGC AGTACTTTTA CATGAACAAG GCGGAGGTGG ATCGGCACCT
 651 GCAGTGCCGT GCCCCGCGCG ATCTCTGCGA GCGCCTGGCG GCGGCCCTGC
 701 GCGAGTCGCC GGGGGCGTCG TTCCGCGGCA TCTCCGCGGA CCACTTCGAG
 35 751 GCGGAGGTGG TGGAGCGCGC CGACGTGTAC TATTACGAAA CGCGCCCGAC
 801 CCTGTACTAC CGCGTCTTCG TGC GAAGCGG GCGCGCGCTG GCCTACCTGT
 40 851 GCGACAACTT TTGCCCCGCG ATCAGGAAGT ACGAGGGGGG CGTCGACGCC
 901 ACCACCCGGT TTATCCTGGA CAACCCGGGG TTTGTACCT TCGGCTGGTA
 951 CCGCCTCAAG CCCGGCCGCG GGAACGCGCC GGCCCAACCG CGCCCCCGA
 45 1001 CGGCGTTCGG AACCTCGAGC GACGTCGAGT TTA ACTGCAC GCGGACAAC
 1051 CTGGCCGTCG AGGGGGCCAT GTGTGACCTG CCGGCCTACA AGCTCATGTG
 50 1101 CTTCGATATC GAATGCAAGG CCGGGGGGGA GGACGAGCTG GCCTTTCCGG
 1151 TCGCGGAACG CCCGGAAGAC CTCGTCATCC AGATCTCCTG TCTGCTCTAC
 1201 GACCTGTCCA CCACCGCCCT CGAGCACATC CTCCTGTTTT CGCTCGGATC
 55 1251 CTGCGACCTC CCCGAGTCCC ACCTCAGCGA TCTCGCCTCC AGGGGCCTGC

1301 CGGCCCCCGT CGTCCTGGAG TTTGACAGCG AATTCGAGAT GCTGCTGGCC
 1351 TTCATGACCT TCGTCAAGCA GTACGGCCCC GAGTTCGTGA CCGGGTACAA
 5 1401 CATCATCAAC TTCGACTGGC CCTTCGTCCT GACCAAGCTG ACGGAGATCT
 1451 ACAAGGTCCC GCTCGACGGG TACGGGCGCA TGAACGGCCG GGGTGTGTTC
 1501 CGCGTGTGGG ACATCGGCCA GAGCCACTTT CAGAAGCGCA GCAAGATCAA
 10 1551 GGTGAACGGG ATGGTGAACA TCGACATGTA CGGCATCATC ACCGACAAGG
 1601 TCAAACCTCTC CAGCTACAAG CTGAACGCCG TCGCCGAGGC CGTCTTGAAG
 15 1651 GACAAGAAGA AGGATCTGAG CTACCGCGAC ATCCCCGCCT ACTACGCCTC
 1701 CGGGCCCGCG CAGCGCGGGG TGATCGGCGA GTATTGTGTG CAGGACTCGC
 1751 TGCTGGTTCG GCAGCTGTTC TTCAAGTTTC TGCCGCACCT GGAGCTTTCC
 20 1801 GCCGTCGCGC GCCTGGCGGG CATCAACATC ACCCGCACCA TCTACGACGG
 1851 CCAGCAGATC CGCGTCTTCA CGTGCCTCCT GCGCCTTGCG GGCCAGAAGG
 25 1901 GCTTCATCCT GCCGGACACC CAGGGGCGGT TTCGGGGCCT CGACAAGGAG
 1951 GCGCCCAAGC GCCCGGCCGT GCCTCGGGGG GAAGGGGAGC GGCCGGGGGA
 2001 CGGGAACGGG GACGAGGATA AGGACGACGA CGAGGACGAG GACGGGGACG
 30 2051 AGCGCGAGGA GGTCGCGCGC GAGACCGGGG GCCGGCACGT TGGGTACCAG
 2101 GGGGCCCCGG TCCTCGACCC CACCTCCGGG TTTCACGTG ACCTCGTGGT
 35 2151 GGTGTTTGAC TTTGCCAGCC TGTACCCAG CATCATCCAG GCCCACAACC
 2201 TGTGCTTCAG TACGCTCTCC CTGCGGCCCG AGGCCGTCGC GCACCTGGAG
 2251 GCGGACCGGG ACTACCTGGA GATCGAGGTG GGGGGCCGAC GGCTGTTCTT
 40 2301 CGTGAAGGCC CACGTACGCG AGAGCCTGCT GAGCATCCTG CTGCGCGACT
 2351 GGCTGGCCAT GCGAAAGCAG ATCCGCTCGC GGATCCCCCA GAGCACCCCC
 45 2401 GAGGAGGCCG TCCTCCTCGA CAAGCAACAG GCCGCCATCA AGGTGGTGTG
 2451 CAACTCGGTG TACGGGTTCA CCGGGGCGCA GCACGGTCTT CTGCCCTGCC
 2501 TGCACGTGGC CGCCACCGTG ACGACCATCG GCCGCGAGAT GCTCCTCGCG
 50 2551 ACGCGCGCGT ACGTGACGC GCGCTGGGCG GAGTTCGATC AGCTGCTGGC
 2601 CGACTTTCCG GAGGCGGCCG GCATGCGCGC CCCCAGTCCG TACTCCATGC
 55 2651 GCATCATCTA CGGGGACACG GACTCCATTT TCGTTTTGTG CCGCGGCCTC
 2701 ACGGCCGCGG GCCTGGTGGC CATGGGCGAC AAGATGGCGA GCCACATCTC
 2751 GCGCGCGCTG TTCCTCCCCC CGATCAAGCT CGAGTGCGAA AAAACGTTCA

2801 CCAAGCTGCT GCTCATCGCC AAGAAAAAGT ACATCGGCGT CATCTGCGGG
2851 GGCAAGATGC TCATCAAGGG CGTGGATCTG GTGCGCAAAA ACAACTGCGC
5 2901 GTTTATCAAC CGCACCTCCA GGGCCCTGGT CGACCTGCTG TTTTACGACG
2951 ATACCGTATC CGGAGCGGCC GCCGCGTTAG CCGAGCGCCC CGCAGAGGAG
10 3001 TGGCTGGCGC GACCCCTGCC CGAGGGACTG CAGGCGTTCG GGGCCGTCTT
3051 CGTAGACGCC CATCGGCGCA TCACCGACCC GGAGAGGGAC ATCCAGGACT
3101 TTGTCCTCAC CGCCGAACTG AGCAGACACC CGCGCGCGTA CACCAACAAG
15 3151 CGCCTGGCCC ACCTGACGGT GTATTACAAG CTCATGGCCC GCCGCGCGCA
3201 GGTCCCGTCC ATCAAGGACC GGATCCCGTA CGTGATCGTG GCCCAGACCC
20 3251 GCGAGGTAGA GGAGACGGTC GCGCGGCTGG CCGCCCTCCG CGAGCTAGAC
3301 GCCGCCGCCC CAGGGGACGA GCCCGCCCCC CCAGCGGCCC TGCCCTCCCC
3351 GGCCAAGCGC CCCCAGGAGA CGCCGTCGCA TGCCGACCCC CCGGGAGGCG
25 3401 CGTCCAAGCC CCGCAAGCTG CTGGTGTCCG AGCTGGCGGA GGATCCCGGG
3451 TACGCCATCG CCCGGGGCGT TCCGCTCAAC ACGGACTATT ACTTCTCGCA
30 3501 CCTGCTGGGG GCGGCCTGCG TGACGTTCAA GGCCCTGTTT GGAAATAACG
3551 CCAAGATCAC CGAGAGTCTG TTAAAGAGGT TTATTCCCGA GACGTGGCAC
3601 CCCCCGGACG ACGTGGCCGC GCGGCTCAGG GCCGCGGGGT TCGGGCCGGC
35 3651 GGGGGCCGGC GCTACGGCGG AGGAAACTCG TCGAATGTTG CATAGAGCCT
3701 TTGATACTCT AGCATGA
40

SEQ. ID. NO. 2 Amino acid sequence of DNA polymerase for HSV2-MS-M1

1 MFCAAGGPTS PGGKSAARAA SGFFAPHNPR GATQTAPPPC RRQNFYNPHL
 5 51 AQTGTQPKAP GPAQRHTYYS ECDEFRIAP RSLDEDAPAE QRTGVHDGRL
 101 RRAPKVYCGG DERDVLRVGP EGFWRRLRL WGGADHAPKG FDPTVTVFHV
 151 YDILEHVEHA YSMRAAQLHE RFMDAITPAG TVITLLGLTP EGHRAVAVHY
 10 201 GTRQYFYMNK AEVDRHLQCR APRDLCERLA AALRESPGAS FRGISADHFE
 251 AEVVERADVY YYETRPTLYY RVFVRSRAL AYLCDNFCPA IRKYEGGVDA
 15 301 TTRFILDNPG FVTFGWYRLK PGRGNAPAP RPPTAFGTSS DVEFNCTADN
 351 LAVEGAMCDL PAYKLMCFDI ECKAGGEDEL AFPVAERPED LVIQISCLLY
 401 DLSTTALEHI LLFSLGSCDL PESHLSDLAS RGLPAPVVLE FDSEFEMLLA
 20 451 FMTFVKQYGP EFVTGYNIN FDWPFVLTKL TEIYKVPLDG YGRMNGRGVF
 501 RVWDIGQSHF QKRSKIKNVNG MVNIDMYGII TDKVKLSSYK LNAVAEAVLK
 25 551 DKKKDLSDYRD IPAYYASGPA QRGVIGEYCV QDSSLVGQLF FKFLPHLELS
 601 AVARLAGINI TRTIYDGQOI RVFTCLLRLA GQKGFILPDT QGRFRGLDKE
 651 APKRAVPRG EGERPGDGNG DEDKDDDEDE DGDEREVAR ETGGRHVGYQ
 30 701 GARVLDPTSG FHVDPVVVFD FASLYPSIIQ AHNLCFSTLS LRPEAVAHLE
 751 ADRDYLEIEV GGRRLFFVKA HVRESLLSIL LRDWLAMRKQ IRSRIPQSTP
 35 801 EEAVLLDKQQ AAIKVCNSV YGFTGAQHGL LPCLHVAATV TTIGREMLLA
 851 TRAYVHARWA EFDQLLADFP EAAGMRAPGP YSMRIYGDT DSIFVLCRGL
 901 TAAGLVAMGD KMASHISRAL FLPPIKLECE KTFTKLLLIA KKKYIGVICG
 40 951 GKMLIKGVDL VRKNNCAFIN RTSRALVDLL FYDDTVSGAA AALAERPAEE
 1001 WLARPLPEGL QAFGAVLVDA HRRITDPERD IQDFVLTAEL SRHPRAYTNK
 45 1051 RLAHLTVYYK LMARRAQVPS IKDRIPYVIV AQTREVEETV ARLAALRELD
 1101 AAPGDEPAP PAALPSPAKR PRETPSHADP PGGASKPRKL LVSELAEDPG
 1151 YAIARGVPLN TDYYFSHLLG AACVTFKALF GNNAKITESL LKRFPETWH
 50 1201 PPDDVAARLR AAGFGPAGAG ATAEETRRML HRAFDTLA*

SEQ.ID.NO. 3 DNA sequence of DNA polymerase gene for HSV2-186-M1

1 ATGTTTTGTG CCGCGGGCGG CCCGGCTTCC CCCGGGGGGA AGTCGGCGGC
 5 51 TCGGGCGGCG TCTGGGTTTT TTGCCCCCA CAACCCCGG GGAGCCACCC
 101 AGACGGCACC GCCGCCTTGC CGCCGGCAGA ACTTCTACAA CCCCCACCTC
 151 GCTCAGACCG GAACGCAGCC AAAGGCCCCC GGGCCGGCTC AGCGCCATAC
 10 201 GTACTACAGC GAGTGCGACG AATTTCGATT TATCGCCCCG CGTTCGCTGG
 251 ACGAGGACGC CCCCGCGGAG CAGCGCACCG GGGTCCACGA CGGCCGCCTC
 15 301 CGGCGCGCCC CTAAGGTGTA CTGCGGGGGG GACGAGCGCG ACGTCCTCCG
 351 CGTGGGCCCC GAGGGCTTCT GGCCGCGTCG CTTGCGCCTG TGGGGCGGTG
 401 CGGACCATGC CCCCGAGGGG TTCGACCCA CCGTCACCGT CTTCCACGTG
 20 451 TACGACATCC TGGAGCACGT GGAACACGCG TACAGCATGC GCGCCGCCCA
 501 GCTCCACGAG CGATTTATGG ACGCCATCAC GCCCGCCGGG ACCGTCATCA
 25 551 CGCTTCTGGG TCTGACCCCC GAAGGCCATC GCGTCGCCGT TCACGTCTAC
 601 GGCACGCGGC AGTACTTTTA CATGAACAAG GCGGAGGTGG ATCGGCACCT
 651 GCAGTGCCGT GCCCCGCGCG ATCTCTGCGA GCGCCTGGCG GCGGCCCTGC
 30 701 GCGAGTCGCC GGGGGCGTCG TTCCGCGGCA TCTCCGCGGA CCACTTCGAG
 751 GCGGAGGTGG TGGAGCGCGC CGACGTGTAC TATTACGAAA CGCGCCCGAC
 35 801 CCTGTACTAC CGCGTCTTCG TGCGAAGCGG GCGCGCGCTG GCCTACCTGT
 851 GCGACAATT TTGCCCCGCG ATCAGGAAGT ACGAGGGGGG CGTCGACGCC
 901 ACCACCCGGT TTATCCTGGA CAACCCGGGG TTTGTACCT TCGGCTGGTA
 40 951 CCGCCTCAAG CCCGGCCGCG GGAACGCGCC GGCCCAACCG CGCCCCCGA
 1001 CGGCGTTCGG AACCTCGAGC GACGTCGAGT TTAAGTGCAC GGCGGACAAC
 45 1051 CTGGCCGTCG AGGGGGCCAT GTGTGACCTG CCGGCCTACA AGCTCATGTG
 1101 CTTGATATC GAATGCAAGG CCGGGGGGGA GGACGAGCTG GCCTTTCCGG
 1151 TCGCGGAACG CCCGGAAGAC CTCGTCATCC AGATCTCCTG TCTGCTCTAC
 50 1201 GACCTGTCCA CCACCGCCCT CGAGCACATC CTCCTGTTTT CGCTCGGATC
 1251 CTGCGACCTC CCCGAGTCCC ACCTCAGCGA TCTCGCCTCC AGGGGCCTGC
 55 1301 CGGCCCCCGT CGTCCTGGAG TTTGACAGCG AATTCGAGAT GCTGCTGGCC
 1351 TTCATGACCT TCGTCAAGCA GTACGGCCCC GAGTTCGTGA CCGGGTACAA
 1401 CATCATCAAC TTCGACTGGC CCTTCGTCCT GACCAAGCTG ACGGAGATCT

1451 ACAAGGTCCC GCTCGACGGG TACGGGCGCA TGAACGGCCG GGGTGTGTTC
 1501 CGCGTGTGGG ACATCGGCCA GAGCCACTTT CAGAAGCGCA GCAAGATCAA
 5 1551 GGTGAACGGG ATGGTGAACA TCGACATGTA CGGCATCATC ACCGACAAGG
 1601 TCAAACCTCTC CAGCTACAAG CTGAACGCCG TCGCCGAGGC CGTCTTGAAG
 10 1651 GACAAGAAGA AGGATCTGAG CTACCGCGAC ATCCCCGCCT ACTACGCCTC
 1701 CGGGCCCCGCG CAGCGCGGGG TGATCGGCGA GTATTGTGTG CAGGACTCGC
 1751 TGCTGGTCGG GCAGCTGTTC TTCAAGTTTC TGCCGCACCT GGAGCTTTCC
 15 1801 GCCGTCGCGC GCCTGGCGGG CATCAACATC ACCCGCACCA TCTACGACGG
 1851 CCAGCAGATC CGCGTCTTCA CGTGCCTCCT GCGCCTTGCG GGCCAGAAGG
 20 1901 GCTTCATCCT GCCGGACACC CAGGGGCGGT TTCGGGGCCT CGACAAGGAG
 1951 GCGCCCAAGC GCCCGGCCGT GCCTCGGGGG GAAGGGGAGC GGCCGGGGGA
 2001 CGGGAACGGG GACGAGGATA AGGACGACGA CGAGGACGGG GACGAGGACG
 25 2051 GGGACGAGCG CGAGGAGGTC GCGCGCGAGA CCGGGGGCCG GCACGTTGGG
 2101 TACCAGGGGG CCCGGGTCCT CGACCCACCT TCCGGGTTTC ACGTCGACCC
 30 2151 CGTGGTGGTG TTTGACTTTG CCAGCCTGTA CCCCAGCATC ATCCAGGCCC
 2201 ACAACCTGTG CTTCAGTACG CTCTCCCTGC GGCCCGAGGC CGTCGCGCAC
 2251 CTGGAGGCGG ACCGGGACTA CCTGGAGATC GAGGTGGGGG GCCGACGGCT
 35 2301 GTTCTTCGTG AAGGCCACG TACGCGAGAG CCTGCTGAGC ATCCTGCTGC
 2351 GCGACTGGCT GGCCATGCGA AAGCAGATCC GCTCGCGGAT CCCCCAGAGC
 40 2401 CCCCCGAGG AGGCCGTCCT CCTCGACAAG CAACAGGCCG CCATCAAGGT
 2451 GGTGTGCAAC TCGGTGTACG GGTTCACCGG GCGCGAGCAC GGTCTTCTGC
 2501 CCTGCCTGCA CGTGGCCGCC ACCGTGACGA CCATCGGCCG CGAGATGCTC
 45 2551 CTCGCGACGC GCGCGTACGT GCACGCGCGC TGGGCGGAGT TCGATCAGCT
 2601 GCTGGCCGAC TTCCGGAGG CGGCCGGCAT GCGCGCCCCC GGTCCGTACT
 50 2651 CCATGCGCAT CATCTACGGG GACACGGACT CCATTTTCGT TTTGTGCCGC
 2701 GGCTCACGG CCGCGGGCCT GGTGGCCATG GCGACAAGA TGGCGAGCCA
 2751 CATCTCGCGC GCGCTGTTC TCCCCCGAT CAAGCTCGAG TGCGAAAAA
 55 2801 CGTTCACCAA GCTGCTGCTC ATCGCCAAGA AAAAGTACAT CGGCGTCATC
 2851 TGCGGGGGCA AGATGCTCAT CAAGGGCGTG GATCTGGTGC GCAAAAACAA

2901 CTGCGCGTTT ATCAACCGCA CCTCCAGGGC CCTGGTCGAC CTGCTGTTTT
2951 ACGACGATAC CGTATCCGGA GCGGCCGCCG CGTTAGCCGA GCGCCCCGCA
5 3001 GAGGAGTGGC TGGCGCGACC CCTGCCCCGAG GGA CTGCAGG CGTTCGGGGC
3051 CGTCCTCGTA GACGCCCATC GGCGCATCAC CGACCCGGAG AGGGACATCC
3101 AGGACTTTGT CCTCACCGCC GAACTGAGCA GACACCCGCG CGCGTACACC
10 3151 AACAAGCGCC TGGCCACCT GACGGTGTAT TACAAGCTCA TGGCCCCGCC
3201 CGCGCAGGTC CCGTCCATCA AGGACCGGAT CCCGTACGTG ATCGTGGCCC
15 3251 AGACCCGCGA GGTAGAGGAG ACGGTCGCGC GGCTGGCCGC CCTCCGCGAG
3301 CTAGACGCCG CCGCCCCAGG GGACGAGCCC GCGCCCCCAG CGGCCCTGCC
3351 CTCCCCGGCC AAGCGCCCCC GGGAGACGCC GTCGCATGCC GACCCCCCGG
20 3401 GAGGCGCGTC CAAGCCCCGC AAGCTGCTGG TGTCCGAGCT GGCGGAGGAT
3451 CCCGGGTACG CCATCGCCCG GGGCGTTCCG CTCAACACGG ACTATTACTT
25 3501 CTCGCACCTG CTGGGGGCGG CCTGCGTGAC GTTCAAGGCC CTGTTTGGA
3551 ATAACGCCAA GATCACCGAG AGTCTGTAA AGAGGTTTAT TCCCGAGACG
3601 TGGCACCCCC CGGACGACGT GGCCGCGCGG CTCAGGGCCG CGGGGTTCGG
30 3651 GCCGGCGGGG GCCGGCGCTA CGGCGGAGGA AACTCGTCGA ATGTTGCATA
3701 GAGCCTTTGA TACTCTAGCA TGA
35

SEQ.ID.NO. 4 Amino acid sequence of DNA polymerase for HSV2-186-M1

5 1 MFCAAGGPAS PGGKSAARAA SGFFAPHNPR GATQTAPPPC RRQNFYNPHL
 51 AQTGTQPKAP GPAQRHTYYS ECDEFRIAP RSLDEDAPAE QRTGVHDGRL
 101 RRAPKVYCGG DERDVLRVGP EGFWRRLRL WGGADHAPEG FDPTVTVFHV
 10 151 YDILEHVEHA YSMRAAQLHE RFMDAITPAG TVITLLGLTP EGHRVAVHVV
 201 GTRQYFYMNK AEVDRHLQCR APRDLCERLA AALRESPGAS FRGISADHFE
 251 AEVVERADVY YYETRPTLYY RVFVRSGRAL AYLCDNFCEA IRKYEGGVDA
 15 301 TTRFILDNPG FVTFGWYRLK PGRGNAPAP RPPTAFGTSS DVEFNCTADN
 351 LAVEGAMCDL PAYKLMCFDI ECKAGGEDEL AFPVAERPED LVIQISCLLY
 20 401 DLSTTALEHI LLFSLGSCDL PESHLSDLAS RGLPAPVVLE FDSEFEMLLA
 451 FMTFVKQYGP EFVTGYNIN FDWPFVLTKL TEIYKVPLDG YGRMNNGRGVF
 501 RVWDIGQSHF QKRSEKIVNG MVNIDMYGII TDKVKLSSYK LNAVAEAVLK
 25 551 DKKKDLSEYD IPAYYASGPA QRGVIGEYCV QDSLLVGQLF FKFLPHLELS
 601 AVARLAGINI TRTIYDGQOI RVFTCLLRLA GQKGFILPDT QGRFRGLDKE
 30 651 APKRPVPRG EGERPGDGNG DEDKDDDEDG DEDGDREEV ARETGGRHVG
 701 YQGARVLDPT SGFHVDPVVV FDFASLYPSI IQAHNLCFST LSLRPEAVAH
 751 LEARDYLEI EVGGRRLLFFV KAHVRESLLS ILLRDWLAMR KQIRSRIPQS
 35 801 PPEEAVLLDK QQAIAKVVCN SVYGFTGAQH GLLPCLHVAA TVTTIGREML
 851 LATRAYVHAR WAEFDQLLAD FPEAAGMRAP GPYSMRIYG DTDSIFVLCR
 40 901 GLTAAGLVAM GDKMASHIS ALFLPIKLE CEKTFTKLLL IAKKKYIGVI
 951 CGGKMLIKGV DLVRKNNCAF INRTSRALVD LLFYDDTVSG AAAALAERPA
 1001 EEWLARPLPE GLQAFGAVLV DAHRRITDPE RDIQDFVLTA ELSRHPRAYT
 45 1051 NKRLAHLTVY YKLMARRAQV PSIKDRIPYV IVAQTREVEE TVARLAALRE
 1101 LDAAAPGDEP APPAALPSA KRPRETSHA DPPGGASKPR KLLVSELAED
 50 1151 PGYAIARGVP LNTDYYFSHL LGAACVTFKA LFGNNAKITE SLLKRFIPET
 1201 WHPPDDVAAR LRAAGFGPAG AGATAEETRR MLHRAFDTLA *

55

SEQ.ID.NO. 5 DNA sequence of DNA polymerase gene for HSV1-KOS-M1

1 ATGTTTTC CG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC
 101 GGGGACCCCC GCCTTGTTTG AGGCAAACT TTTACAACCC CTACCTCGCC
 151 CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA
 10 201 CTATAGCGAA TGCATGAAT TTCGATTCAT CGCCCCGCGG GTGCTGGACG
 251 AGGATGCCCC CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG
 15 301 CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCCTCCGCGT
 351 CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GGCGGCGTGG
 401 ACCACGCCCC GCGGGGGTTC AACCCACCG TCACCGTCTT TCACGTGTAC
 20 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCAGTT
 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC
 25 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTTACGGC
 601 ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTTGACA GGCACCTACA
 651 ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG
 30 701 AGTCCCCGGG CGCGTCGTTC CGCGGCATCT CCGCGGACCA CTTCGAGGGC
 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT
 35 801 GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTCG TACCTGTGCG
 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC
 901 ACCCGGTTCA TCCTGGACAA CCCC GG GTTC GTCACCTTCG GCTGGTACCG
 40 951 TCTCAAACCG GGCCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG
 1001 CCTTCGGGAC ATCCAGCGAC GTCGAGTTTA ACTGTACGGC GGACAACCTG
 45 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT
 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG
 1151 CCGGGCACCC GGAGGACCTG GTTATTCAGA TATCCTGTCT GCTCTACGAC
 50 1201 CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTTCGC TCGGTTCTTG
 1251 CGACCTCCCC GAATCCCACC TGAACGAGCT GCGGCCAGG GGCCTGCCCA
 55 1301 CGCCCGTGGT TCTGGAATTC GACAGCGAAT TCGAGATGCT GTTGGCCTTC
 1351 ATGACCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT
 1401 CATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGTTGACG GACATTTACA

1451 AGGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTTTCGC
 1501 GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT
 5 1551 GAACGGCATG GTGAACATCG ACATGTACGG GATCATAACC GACAAGATCA
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC
 10 1651 AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCGCCTACT ACGCCGCCGG
 1701 GCCCGCGCAA CGCGGGGTGA TCGGCGAGTA CTGCATACAG GATTCCCTGC
 1751 TGGTGGGCCA GCTGTTTTTT AAGTTTTTGC CCCATCTGGA GCTCTCGGCC
 15 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA
 1851 GCAGATCCGC GTCTTTACGT GCCTGCTGCG CCTGGCCGAC CAGAAGGGCT
 20 1901 TTATTCTGCC GGACACCCAG GGGCGATTTA GGGGCGCCGG GGGGGAGGCG
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA
 2001 GGGGGAGGAC GAGGACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG
 25 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG
 2101 GTCCTTGACC CCACTTCCGG GTTTCACGTG AACCCCGTGG TGGTGTTCGA
 30 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCACAAC CTGTGCTTCA
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG
 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC
 35 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC
 40 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACCTCGGT
 2451 GTACGGGTTC ACGGGAGCGC AGCACGGA CTGCGCGTGC CTGCACGTTG
 2501 CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG
 45 2551 TACGTCCACG CGCGCTGGGC GGCCTTCGAA CAGCTCCTGG CCGATTTCCT
 2601 GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT
 50 2651 ACGGGGACAC GGACTCCATA TTTGTGCTGT GCCGCGGCCT CACGGCCGCC
 2701 GGGCTGACGG CCATGGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT
 2751 GTTTCTGCCC CCCATCAAAC TCGAGTGCGA AAAGACGTTC ACCAAGCTGC
 55 2801 TGCTGATCGC CAAGAAAAAG TACATCGGCG TCATCTACGG GGGTAAGATG
 2851 CTCATCAAGG GCGTGGATCT GGTGCGCAAA AACAACTGCG CGTTTATCAA

2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTTACGAC GATACCGTAT
2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG
5 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC
3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTCCTCA
3101 CCGCCGA ACT GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC
10 3151 CACCTGACGG TGTATTACAA GCTCATGGCC CGCCGCGCGC AGGTCCCCTC
3201 CATCAAGGAC CGGATCCCGT ACGTGATCGT GGCCCAGACC CGCGAGGTAG
15 3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTAGA CGCCGCCCGC
3301 CCAGGGGACG AGCCCGCCCC CCCC GCGGCC CTGCCCTCCC CGGCCAAGCG
3351 CCCCCGGGAG ACGCCGTCGC ATGCCGACCC CCCGGGAGGC GCGTCCAAGC
20 3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCCGC ATACGCCATT
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG
25 3501 GGCGGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCGGAC
3601 GACGTGGCCG CGCGGCTCCG GGCCGCAGGG TTCGGGGCGG TGGGTGCCGG
30 3651 CGCTACGGCG GAGGAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC
3701 TAGCATGA

35

SEQ.ID.NO. 6 Amino acid sequence of DNA polymerase for HSV1-KOS-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPPCL RQNFYNPYLA
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPEK RAGVHDGHLK
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY
 10 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVY
 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCPAI KKYEGGV DAT
 15 301 TRFILDNPGF VTFGWYRLKP GRNNTLAQPR APMAFGTSSD VEFNCTADNL
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD
 20 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF
 451 MTLVKQYGPE FVTGYNIINF DWPFLAKLT DIYKVPLDGY GRMN GRGVFR
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVAEAVLKD
 25 551 KKKDLSYRDI PAYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA
 601 VARLAGINIT RTIYDGQQIR VFTCLRLAD QKGFILPDTQ GRFRGAGGEA
 30 651 PKRPAAARED EERPEEEGED EDEREEGGGE REPEGARETA GRHVG YQGAR
 701 VLDPTSGFHV NPVVVFDFAS LYPSIIQAHN LCFSTLSLRA DAVAHLEAGK
 751 DYLEIEVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA
 35 801 VLLDKQQA AI KVCNSVYGF TGAQHGLLPC LHVAATVTTI GREMLLATRE
 851 YVHARWAAFE QLLADFPEAA DMRAPGPYSM RIYGD TDSI FVLCRGLTAA
 40 901 GLTAMGDKMA SHISRALFLP PIKLECEKTF TKLLLIAKKK YIGVIYGGKM
 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERP AEEWLA
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA
 45 1051 HLTVYYKLMA RRAQVPSIKD RPYVIVAQT REVEETVARL AALRELDAAA
 1101 PGDEPAPPAA LPSPAKRPRE TPSHADPPGG ASKPRKLLVS ELAEDPAYAI
 50 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD
 1201 DVAARLRAAG FGAVGAGATA EETRRMLHRA FDTLA*

SEQ.ID.NO. 7 DNA sequence of HSV polymerase gene for HSV1-F-M1

```

5      1  ATGTTTTCCG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC
      51  CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC
     101  GGGGACCCCC GCCTTGCTTG AGGCAAAACT TTTACAACCC CTACCTCGCC
10     151  CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA
      201  CTATAGCGAA TCGATGAAT TTCGATTCAT CGCCCCGCGG GTGCTGGACG
      251  AGGATGCCCC CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG
15     301  CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCC'TCCGCGT
      351  CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GCGGCGGTGG
     20  401  ACCACGCCCC GCGGGGGTTC AACCCACCG TCACCGTCTT TCACGTGTAC
      451  GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCCAGTT
      501  CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC
25     551  TCCTGGGCCT GACTCCGGA GGCCACCGGG TGGCCGTTC ACGTTTACGGC
      601  ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTCGACA GGCACCTACA
     30  651  ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG
      701  AGTCCCCGGG CGCGTCGTTC CGCGGCATTT CCGCGGACCA CTTCGAGGCG
      751  GAGGTGGTGG AGCGCACCGA CGTGTACTION TACGAGACGC GCCCCGCTCT
35     801  GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTG TACCTGTGCG
      851  ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC
     40  901  ACCCGGTTCA TCCTGGACAA CCCCAGGTTC GTCACCTTCG GCTGGTACCG
      951  TCTCAAACCG GGCCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG
     45 1001  CCTTCGGGAC ATCCAGCGAC GTCGAGTTTA ACTGTACGGC GGACAACCTG
      1051  GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT
     50 1101  CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG
      1151  CCGGGCACCC GGAGGACCTG GTCATCCAGA TATCCTGTCT GCTCTACGAC
      1201  CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTTTCG TCGGTTCCCTG
      1251  CGACCTCCCC GAATCCCACC TGAACGAGCT GGCGGCCAGG GGCCTGCCCA
55     1301  CGCCCGTGGT TCTGGAATTC GACAGCGAAT TCGAGATGCT GTTGGCCTTC
      1351  ATGACCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT
     60 1401  CATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGCTGACG GACATTTACA
      1451  AGGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTTTCG
      1501  GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT

```

1551 GAACGGCATG GTGAACATCG ACATGTACGG GATTATAACC GACAAGATCA
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC
 5 1651 AAGAAGAAAG ACCTGAGCTA TCGCGACATC CCCGCCTACT ACGCCGCCGG
 1701 GCCCGCGCAA CGCGGGGTGA TCGCGAGTA CTGCATACAG GATTCCCTGC
 10 1751 TGGTGGGCCA GCTGTTTTTT AAGTTTTTGC CCCATCTGGA GCTCTCGGCC
 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA
 1851 GCAGATCCGC GTCTTTACGT GCGTGC'TGCG CCTGGCCGAC CAGAAGGGCT
 15 1901 TTAT'TCTGCC GGACACCCAG GGGCGATTTA GGGGCGGCGG GGGGGAGGCG
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA
 20 2001 GGGGGAGGAC GAGGACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG
 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG
 2101 GTCCTTGACC CCACTTCCGG GTTTCATGTG AACCCCGTGG TGGTGTTCGA
 25 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCACAAC CTGTGCTTCA
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG
 30 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC
 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC
 35 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACTCGGT
 2451 TTACGGGTTC ACGGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG
 40 2501 CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG
 2551 TACGTCCACG CGCGCTGGGC GGCCTTCGAA CAGCTCCTGG CCGATTTCCC
 2601 GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT
 45 2651 ACGGGGACAC GGACTCCATC TTTGTGCTGT GCCGCGGCCT CACGGCCGCC
 2701 GGGCTGACGG CCGTGGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT
 50 2751 GTTCTGTGCC CCCATCAAAC TCGAGTGCGA AAAGACGTTT ACCAAGCTGC
 2801 TGCTGATCGC CAAGAAAAAG TACATCGGCG TCATCTACGG GGGTAAGATG
 2851 CTCATCAAGG GCGTGGATCT GGTGCGCAAA AACAAC'TGCG CGTTTATCAA
 55 2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTTACGAC GATACCGTAT
 2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG
 60 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC
 3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTCCTCA
 3101 CCGCCGA'ACT GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC
 65

| | | | | | | |
|----|------|------------|-------------|------------|------------|-------------|
| | 3151 | CACCTGACGG | TGTATTACAA | GTCATGGCC | CGCCGCGCGC | AGGTCCCCGTC |
| | 3201 | CATCAAGGAC | CGGATCCCCGT | ACGTGATCGT | GGCCCAGACC | CGCGAGGTAG |
| 5 | 3251 | AGGAGACGGT | CGCGCGGCTG | GCCGCCCTCC | GCGAGCTCGA | CGCCGCCGCC |
| | 3301 | CCAGGGGACG | AGCCCGCCCC | CCCCGCGGCC | CTGCCCTCCC | CGGCCAAGCG |
| | 3351 | CCCCCGGGAG | ACGCCGTTGC | ATGCCGACCC | CCCGGGAGGC | GCGTCCAAGC |
| 10 | 3401 | CCCGCAAGCT | GCTGGTGTCC | GAGCTGGCCG | AGGATCCCCG | ATACGCCATT |
| | 3451 | GCCCACGGCG | TCGCCCTGAA | CACGGACTAT | TACTTCTCCC | ACCTGTTGGG |
| 15 | 3501 | GGCGGCGTGC | GTGACATTCA | AGGCCCTGTT | TGGGAATAAC | GCCAAGATCA |
| | 3551 | CCGAGAGTCT | GTTAAAAAGG | TTTATTCCCC | AAGTGTGGCA | CCCCCGGAC |
| | 3601 | GACGTGGCCG | CGCGGCTCCG | GGCCGCAGGG | TTCGGGGCGG | TGGGTGCCGG |
| 20 | 3651 | CGCTACGGCG | GAGGAAACTC | GTCGAATGTT | GCATAGAGCC | TTTGATACTC |
| | 3701 | TAGCATGA | | | | |

SEQ.ID.NO. 8 Amino acid sequence of DNA polymerase for HSV1-F-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPPCL RQNFYNPYLA
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPEK RAGVHDGHLK
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY
 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVY
 10 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA
 251 EVVERTDVYY YETRPALFYR VYVRSRVLV YLCDNFCPAI KKYEGGV DAT
 15 301 TRFILDNPGF VTFGWYRLKP GRNNTLAQPR APMAFGTSSD VEFNCTADNL
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD
 401 LSTTALEHVL LFSLGSCDLP ESHLNELAA RGLPTPVVLEF DSEFEMLLAF
 20 451 MTLVKQYGPE FVTGYNINIF DWPFLAKLT DIYKVPLDGY GRMNRRGVFR
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVA EAVLKD
 25 551 KKKDLSYRDI PAYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA
 601 VARLAGINIT RTIYDGQQIR VFTCLRLAD QKGFILPDTQ GRFRGGGGEA
 651 PKRPAAARED EERPEEEGED EDEREEGGGE REPEGARETA GRHVGYQGAR
 30 701 VLDPTSGFHV NPVVVFDFAS LYPSIIQAHN LCFSTLSLRA DAVAHLEAGK
 751 DYLEIEVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA
 35 801 VLLDKQQA AIKVCNSVYGF TGAQHGLLPC LHVAATVTTI GREMLLATRE
 851 YVHARWAAFE QLLADFPEAA DMRAPGPYSM RIYGD TDSI FVLCRGLTAA
 901 GLTAVGDKMA SHISRALFLS PIKLECEKTF TKLLLIAKKK YIGVIYGGKM
 40 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAEEWLA
 1001 RPLPEGLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA
 45 1051 HLTVYYKLMA RRAQVPSIKD RPYVIVAQT REVEETVARL AALRELDAAA
 1101 PGDEPAPPAA LPSPAKRPRE TPLHADPPGG ASKPRKLLVS ELAEDPAYAI
 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD
 50 1201 DVAARLRAAG FGAVGAGATA EETRMLHRA FDTLA*

SEQ.ID.NO. 9 DNA sequence of HSV polymerase gene for HSV1-DJL-M1

1 ATGTTTTCCG GTGGCGGCGG CCCGCTGTCC CCCGGAGGAA AGTCGGCGGC
 5 51 CAGGGCGGCG TCCGGGTTTT TTGCGCCCGC CGGCCCTCGC GGAGCCGGCC
 101 GGGGACCCCC GCCTTGTTTG AGGCAAACT TTTACAACCC CTACCTCGCC
 151 CCAGTCGGGA CGCAACAGAA GCCGACCGGG CCAACCCAGC GCCATACGTA
 10 201 CTATAGCGAA TCGATGAAT TTCGATTCAT CGCCCCGCGG GTGCTGGACG
 251 AGGATGCCCC CCCGGAGAAG CGCGCCGGGG TGCACGACGG TCACCTCAAG
 15 301 CGCGCCCCCA AGGTGTACTG CGGGGGGGAC GAGCGCGACG TCCTCCGCGT
 351 CGGGTCGGGC GGCTTCTGGC CGCGGCGCTC GCGCCTGTGG GGC GGCGTGG
 401 ACCACGCCCC GGC GGGGTTT AACCACCG TCACCGTCTT TCACGTGTAT
 20 451 GACATCCTGG AGAACGTGGA GCACGCGTAC GGCATGCGCG CGGCCAGTT
 501 CCACGCGCGG TTTATGGACG CCATCACACC GACGGGGACC GTCATCACGC
 25 551 TCCTGGGCCT GACTCCGGAA GGCCACCGGG TGGCCGTTCA CGTTTACGGC
 601 ACGCGGCAGT ACTTTTACAT GAACAAGGAG GAGGTTGACA GGCACCTACA
 651 ATGCCGCGCC CCACGAGATC TCTGCGAGCG CATGGCCGCG GCCCTGCGCG
 30 701 AGTCCCCGGG CGCGTCGTTT CGCGGCATCT CCGCGGACCA CTTCGAGGCG
 751 GAGGTGGTGG AGCGCACCGA CGTGTACTAC TACGAGACGC GCCCCGCTCT
 35 801 GTTTTACCGC GTCTACGTCC GAAGCGGGCG CGTGCTGTCG TACCTGTGCG
 851 ACAACTTCTG CCCGGCCATC AAGAAGTACG AGGGTGGGGT CGACGCCACC
 901 ACCCGGTTCA TCCTGGACAA CCCC GGGTTC GTCACCTTCG GCTGGTACCG
 40 951 TCTCAAACCG GGCCGGAACA ACACGCTAGC CCAGCCGCGG GCCCCGATGG
 1001 CCTTCGGGAC ATCCAGCGAT GTCGAGTTTA ACTGTACGGC GGACAACCTG
 45 1051 GCCATCGAGG GGGGCATGAG CGACCTACCG GCATACAAGC TCATGTGCTT
 1101 CGATATCGAA TGCAAGGCGG GGGGGGAGGA CGAGCTGGCC TTTCCGGTGG
 1151 CCGGGCACCC GGAGGACCTG GTCATCCAGA TATCCTGTCT GCTCTACGAC
 50 1201 CTGTCCACCA CCGCCCTGGA GCACGTCCTC CTGTTTTCGC TCGGTTCTG
 1251 CGACCTCCCC GAATCCCACC TGAACGAGCT GGC GGCCAGG GGCCTGCCA
 55 1301 CGCCCGTGGT TCTGGAATTC GACAGCGAAT TCGAGATGCT GTTGGCCTTC
 1351 ATGACCCTTG TGAAACAGTA CGGCCCCGAG TTCGTGACCG GGTACAACAT

1401 AATCAACTTC GACTGGCCCT TCTTGCTGGC CAAGCTGACG GACATTTACA
 1451 AGGTCCCCCT GGACGGGTAC GGCCGCATGA ACGGCCGGGG CGTGTTTCGC
 5 1501 GTGTGGGACA TAGGCCAGAG CCACTTCCAG AAGCGCAGCA AGATAAAGGT
 1551 GAACGGCATG GTGAACATCG ACATGTACGG GATTATAACC GACAAGATCA
 1601 AGCTCTCGAG CTACAAGCTC AACGCCGTGG CCGAAGCCGT CCTGAAGGAC
 10 1651 AAGAAGAAGG ACCTGAGCTA TCGCGACATC CCCACCTACT ACGCCGCCGG
 1701 GCCCGCGCAA CGCGGGGTGA TCGGCGAGTA CTGCATACAG GATTCCCTGC
 1751 TGGTGGGCCA GCTGTTTTTT AAGTTTTTGC CCCATCTGGA GCTCTCGGCC
 1801 GTCGCGCGCT TGGCGGGTAT TAACATCACC CGCACCATCT ACGACGGCCA
 1851 GCAGATCCGC GTCTTTACGT GCCTGCTGCG CCTGGCCGAC CAGAAGGGCT
 20 1901 TTATTCTGCC GGACACCCAG GGGCGATTTA GGGGCGCCGG GGGGGAGGCG
 1951 CCCAAGCGTC CGGCCGCAGC CCGGGAGGAC GAGGAGCGGC CAGAGGAGGA
 25 2001 GGGGGAGGAC GAGAACGAAC GCGAGGAGGG CGGGGGCGAG CGGGAGCCGG
 2051 AGGGCGCGCG GGAGACCGCC GGCCGGCACG TGGGGTACCA GGGGGCCAGG
 2101 GTCCTTGACC CCACTTCCGG GTTTCACGTG AACCCCGTGG TGGTGTTCTGA
 30 2151 CTTTGCCAGC CTGTACCCCA GCATCATCCA GGCCCACAAC CTGTGCTTCA
 2201 GCACGCTCTC CCTGAGGGCC GACGCAGTGG CGCACCTGGA GGCGGGCAAG
 35 2251 GACTACCTGG AGATCGAGGT GGGGGGGCGA CGGCTGTTCT TCGTCAAGGC
 2301 TCACGTGCGA GAGAGCCTCC TCAGCATCCT CCTGCGGGAC TGGCTCGCCA
 2351 TGCGAAAGCA GATCCGCTCG CGGATTCCCC AGAGCAGCCC CGAGGAGGCC
 40 2401 GTGCTCCTGG ACAAGCAGCA GGCCGCCATC AAGGTCGTGT GTAACCTCGGT
 2451 TTACGGGTTC ACGGGAGCGC AGCACGGACT CCTGCCGTGC CTGCACGTTG
 45 2501 CCGCGACGGT GACGACCATC GGCCGCGAGA TGCTGCTCGC GACCCGCGAG
 2551 TACGTCCACG CGCGCTGGG GGCCTTCGAA CAGCTCCTGG CCGATTTCCT
 2601 GGAGGCGGCC GACATGCGCG CCCCCGGGCC CTATTCCATG CGCATCATCT
 50 2651 ACGGGGACAC GGA CTCCATA TTTGTGCTGT GCCGCGGCCT CACGGCCGCC
 2701 GGGCTGACGG CCGTGGGCGA CAAGATGGCG AGCCACATCT CGCGCGCGCT
 55 2751 GTTTCTGCCC CCCATCAAAC TCGAGTGCGA AAAGACGTTT ACCAAGCTGC
 2801 TGCTGATCGC CAAGAAAAAG TACATCGGCG TCATCTACGG GGGTAAGATG
 2851 CTCATCAAGG GCGTGGATCT GGTGCGCAA AACAACTGCG CGTTTATCAA

2901 CCGCACCTCC AGGGCCCTGG TCGACCTGCT GTTTTACGAC GATACCGTAT
2951 CCGGAGCGGC CGCCGCGTTA GCCGAGCGCC CCGCAGAGGA GTGGCTGGCG
5 3001 CGACCCCTGC CCGAGGGACT GCAGGCGTTC GGGGCCGTCC TCGTAGACGC
3051 CCATCGGCGC ATCACCGACC CGGAGAGGGA CATCCAGGAC TTTGTTCTCA
10 3101 CCGCCGA ACT GAGCAGACAC CCGCGCGCGT ACACCAACAA GCGCCTGGCC
3151 CACCTGACGG TGTATTACAA GTCATGGCC CGCCGCGCGC AGGTCCCGTC
3201 CATCAAGGAC CGGATCCCGT ACGTGATCGT GGCCCAGACC CGCGAGGTAG
15 3251 AGGAGACGGT CGCGCGGCTG GCCGCCCTCC GCGAGCTAGA CGCCGCCGCC
3301 CCAGGGGACG AGCCCGCCCC CCCC GCGGCC CTGCCCTCCC CGGCCAAGCG
20 3351 CCCCCGGGAG ACGCCGTCGC CTGCCGACCC CCCGGGAGGC GCGTCCAAGC
3401 CCCGCAAGCT GCTGGTGTCC GAGCTGGCCG AGGATCCCGC ATACGCCATT
3451 GCCCACGGCG TCGCCCTGAA CACGGACTAT TACTTCTCCC ACCTGTTGGG
25 3501 GGCGGCGTGC GTGACATTCA AGGCCCTGTT TGGGAATAAC GCCAAGATCA
3551 CCGAGAGTCT GTTAAAAAGG TTTATTCCCG AAGTGTGGCA CCCCCGGAC
30 3601 GACGTGGCCG CGCGGCTCCG GACCGCAGGG TTCGGGGCGG TGGGTGCCGG
3651 CGCTACGGCG GAGGAACTC GTCGAATGTT GCATAGAGCC TTTGATACTC
3701 TAGCATGA
35

SEQ.ID.NO. 10 Amino acid sequence of DNA polymerase for HSV1-DJL-M1

1 MFSGGGGPLS PGGKSAARAA SGFFAPAGPR GAGRGPPPCL RQNFYNPYLA
 5 51 PVGTQQKPTG PTQRHTYYSE CDEFRIAPR VLDEDAPEK RAGVHDGHLK
 101 RAPKVYCGGD ERDVLRVGSG GFWPRRSRLW GGVDHAPAGF NPTVTVFHVY
 151 DILENVEHAY GMRAAQFHAR FMDAITPTGT VITLLGLTPE GHRVAVHVY
 10 201 TRQYFYMNKE EVDRHLQCRA PRDLCERMAA ALRESPGASF RGISADHFEA
 251 EVVERTDVYY YETRPALFYR VYVRSGRVLS YLCDNFCAI KKYEGGV DAT
 15 301 TRFILDNPGF VTFGWYRLKP GRNNTLAQPR APMAFGTSSD VEFNCTADNL
 351 AIEGGMSDLP AYKLMCFDIE CKAGGEDELA FPVAGHPEDL VIQISCLLYD
 401 LSTTALEHVL LFSLGSCDLP ESHLNELAAR GLPTPVVLEF DSEFEMLLAF
 20 451 MTLVKQYGPE FVTGYNIINF DWPFLAKLT DIYKVPLDGY GRMNGRGVFR
 501 VWDIGQSHFQ KRSKIKVNGM VNIDMYGIIT DKIKLSSYKL NAVA EAVLKD
 25 551 KKKDLSYRDI PTYYAAGPAQ RGVIGEYCIQ DSLLVGQLFF KFLPHLELSA
 601 VARLAGINIT RTIYDGQQIR VFTCLRLAD QKGFILPDTQ GRFRGAGGEA
 651 PKRPAAARED EERPEEEGED ENERE EGGGE REPEGARETA GRHVG YQGAR
 30 701 VLDPTSGFHV NPVVVFDFAS LYPSIIQAHN LCFSTLSLRA DAVAHLEAGK
 751 DYLEIEVGGR RLFFVKAHVR ESLLSILLRD WLAMRKQIRS RIPQSSPEEA
 35 801 VLLDKQQA AI KVCNSVYGF TGAQHGLLPC LHVAATVT TI GREMLLATRE
 851 YVHARWAAFE QLLADFP EAA DMRAPGPYSM RIYGD TDSI FVLCRGLTAA
 901 GLTAVGDKMA SHISRALFLP PIKLECEKTF TKLLLI AKKK YIGVIYGGKM
 40 951 LIKGVDLVRK NNCAFINRTS RALVDLLFYD DTVSGAAAAL AERPAE EWLA
 1001 RLP EQLQAF GAVLVDAHRR ITDPERDIQD FVLTAELSRH PRAYTNKRLA
 45 1051 HLT VYYKLMA RRAQVPSIKD RPYVIVAQT REVEETVARL AALRELDAAA
 1101 PGDEPAPPAA LPSPAKRPRE TPSPADPPGG ASKPRKLLVS ELAEDPAYAI
 1151 AHGVALNTDY YFSHLLGAAC VTFKALFGNN AKITESLLKR FIPEVWHPPD
 50 1201 DVAARLRTAG FGAVGAGATA EETRRMLHRA FDTLA*

SEQ.ID.NO. 11 DNA sequence of DNA polymerase gene for HMCV-AD169-M1

```

1  ATGTTTTTCA ACCCGTATCT GAGCGGCGGC GTGACCGGCG GTGCGGTCGC
5  51  GGGTGGCCGG CGTCAGCGTT CGCAGCCCGG CTCCGCGCAG GGCTCGGGCA
    101  AGCGGCCGCC ACAGAAACAG TTTTTCGAGA TCGTGCCGCG AGGTGTCATG
    151  TTCGACGGTC AGACGGGGTT GATCAAGCAT AAGACGGGAC GGCTGCCTCT
10  201  CATGTTCTAT CGAGAGATTA AACATTTGTT GAGTCATGAC ATGGTTTGGC
    251  CGTGTCTTGT GCGCGAGACC CTGGTGGGTC GCGTGGTGGG ACCTATTCGT
    301  TTTCACACCT ACGATCAGAC GGACGCCGTG CTCTTCTTCG ACTCGCCCGA
    351  AAACGTGTCT CCGCGCTATC GTCAGCATCT GGTGCCTTCG GGGAACGTGT
    401  TGCGTTTCTT CGGGGCCACA GAACACGGCT ACAGTATCTG CGTCAACGTT
20  451  TTCGGGCAGC GCAGCTACTT TTAAGTGAG TACAGCGACA CCGATAGGCT
    501  GCGTGAGGTC ATTGCCAGCG TGGGCGAACT AGTGCCCGAA CCGCGGACGC
    551  CATA CGCCGT GTCTGTCACG CCGGCCACCA AGACCTCCAT CTATGGGTAC
25  601  GGGACGCGAC CCGTGCCCGA TTTGCAGTGT GTGTCTATCA GCAACTGGAC
    651  CATGGCCAGA AAAATCGGCG AGTATCTGCT GGAGCAGGGT TTTCCCGTGT
    701  ACGAGGTCCG TGTGGATCCG CTGACGCGTT TGGTCATCGA TCGGCGGATC
30  751  ACCACGTTCG GCTGGTGCTC CGTGAATCGT TACGACTGGC GGCAGCAGGG
    801  TCGCGCGTCG ACTTGTGATA TCGAGGTAGA CTGCGATGTC TCTGACCTGG
    851  TGGCTGTGCC CGACGACAGC TCGTGGCCGC GCTATCGATG CCTGTCCTTC
    901  GATATCGAGT GCATGAGCGG CGAGGGTGGT TTTCCCTGCG CCGAGAAGTC
40  951  CGATGACATT GTCATTGAGA TCTCGTGCCT GTGCTACGAG ACGGGGGGAA
    1001  ACACCGCCGT GGATCAGGGG ATCCCAAACG GGAACGATGG TCGGGGCTGC
    1051  ACTTCGGAGG GTGTGATCTT TGGGCACTCG GGTCTTCATC TCTTTACGAT
45  1101  CGGCACCTGC GGGCAGGTGG GCCCAGACGT GGACGTCTAC GAGTTCCTT
    1151  CCGAATACGA GCTGCTGCTG GGCTTTATGC TTTTCTTTCA ACGGTACGCG
50  1201  CCGGCCTTTG TGACCGGTTA CAACATCAAC TCTTTTGACT TGAAGTACAT
    1251  CCTCACGCGT CTCGAGTACC TGTATAAGGT GGAATCGCAG CGCTTCTGCA
    1301  AGTTGCCTAC GGCAGAGGGC GGCCGTTTCT TTTTACACAG CCCC GCCGTG
55  1351  GGTTTTAAGC GGCAGTACGC CGCCGCTTTT CCCTCGGCTT CTCACAACAA

```

1401 TCCGGCCAGC ACGGCCGCCA CCAAGGTGTA TATTGCGGGT TCGGTGGTTA
 1451 TCGACATGTA CCCTGTATGC ATGGCCAAGA CTAACTCGCC CAACTATAAG
 5 1501 CTCAACACTA TGGCCGAGCT TTACCTGCGG CAACGCAAGG ATGACCTGTC
 1551 TTACAAGGAC ATCCCGCGTT GTTTCGTGGC TAATGCCGAG GGCCGCGCCC
 1601 AGGTAGGCCG TTAAGTCTG CAGGACGCCG TATTGGTGCG CGATCTGTTC
 10 1651 AACACCATTA ATTTTCACTA CGAGGCCGGG GCCATCGCGC GGCTGGCTAA
 1701 AATTCCGTTG CGGCGTGTCA TCTTTGACGG ACAGCAGATC CGTATCTACA
 1751 CCTCGCTGCT GGACGAGTGC GCCTGCCGCG ATTTTATCCT GCCCAACCAC
 1801 TACAGCAAAG GTACGACGGT GCCCGAAACG AATAGCGTTG CTGTGTCACC
 1851 TAACGCTGCT ATCATCTCTA CCGCCGCTGT GCCCGGCGAC GCGGGTTCTG
 20 1901 TGGCGGCTAT GTTTCAGATG TCGCCGCCCT TGCAATCTGC GCCGTCCAGT
 1951 CAGGACGGCG TTTCACCCGG CTCCGGCAGT AACAGTAGTA GCAGCGTCGG
 2001 CGTTTTTCAGC GTCGGCTCCG GCAGTAGTGG CGGCGTCGGC GTTTCCAACG
 2051 ACAATCACGG CGCCGGCGGT ACTGCGGCGG TTTCGTACCA GGGCGCCACG
 2101 GTGTTTGAGC CCGAGGTGGG TTAAGTACAAC GACCCCGTGG CCGTGTTCTGA
 30 2151 CTTTGCCAGC CTCTACCCTT CCATCATCAT GGCCCAACAAC CTCTGCTACT
 2201 CCACCCTGCT GGTGCCGGGT GGCAGTAGTACC CTGTGGACCC CGCCGACGTA
 2251 TACAGCGTCA CGCTAGAGAA CGGCGTGACC CACCGCTTTG TGCCTGCTTC
 2301 GGTGCGCGTC TCGGTGCTCT CGGAAGTGT CAACAAGTGG GTTTCGCAGC
 2351 GGCCTGCCGT GCGCGAATGC ATGCGCGAGT GTCAAGACCC TGTGCGCCGT
 40 2401 ATGCTGCTCG ACAAGGAACA GATGGCGCTC AAAGTAACGT GCAACGCTTT
 2451 CTACGGTTTT ACCGGCGCGC TGAACGGTAT GATGCCGTGT CTGCCCATCG
 2501 CCGCCAGCAT CACGCGCATC GGTGCGGACA TGCTAGAGCG CACGGCGCGG
 2551 TTCATCAAAG ACAACTTTTC AGAGCCGTGT TTTTGCACA ATTTTTTTAA
 2601 TCAGGAAGAC TATGTAGTGG GAACGCGGGA GGGGGATTCG GAGGAGAGCA
 50 2651 GCGCGTTACC GGAGGGGCTC GAAACATCGT CAGGGGGCTC GAACGAACGG
 2701 CGGGTGGAGG CGCGGGTCAT CTACGGGGAC ACGGACAGCG TGTTTGTCCG
 2751 CTTTCGTGGC CTGACGCCGC AGGCTCTGGT GGCCTGTGGG CCCAGCCTGG
 2801 CGCACTACGT GACGGCCTGT CTTTTGTGG AGCCCGTCAA GCTGGAGTTT
 2851 GAAAAGGTCT TCGTCTCTCT TATGATGATC TGCAAGAAAC GTTACATCGG

2901 CAAAGTGGAG GGC GCCTCGG GTCTGAGCAT GAAGGGCGTG GATCTGGTGC
2951 GCAAGACGGC CTGCGAGTTC GTCAAGGGCG TCACGCGTGA CGTCCTCTCG
5 3001 CTGCTCTTTG AGGATCGCGA GGTCTCGGAA GCAGCCGTGC GCCTGTCGCG
3051 CCTCTCACTC GATGAAGTCA AGAAGTACGG CGTGCCACGC GGTTCCTGGC
10 3101 GTATCTTACG CCGCTTGGTG CAGGCCCCGCG ACGATCTGTA CCTGCACCGT
3151 GTGCGTGTCG AGGACCTGGT GCTTTCGTCG GTGCTCTCTA AGGACATCTC
3201 GCTGTACCGT CAATCTAACC TGCCGCACAT TGCCGTCATT AAGCGATTGG
15 3251 CGGCCCGTTC TGAGGAGCTA CCCTCGGTCTG GGGATCGGGT CTTTTACGTT
3301 CTGACGGCGC CCGGTGTCCG GACGGCGCCG CAGGGTTCCT CCGACAACGG
20 3351 TGATTCTGTA ACCGCCGGCG TGGTTTCCCG GTCGGACGCG ATTGATGGCA
3401 CGGACGACGA CGCTGACGGC GGC GGGGTAG AGGAGAGCAA CAGGAGAGGA
3451 GGAGAGCCGG CAAAGAAGAG GGCGCGGAAA CCACCGTCGG CCGTGTGCAA
25 3501 CTACGAGGTA GCCGAAGATC CGAGCTACGT GCGCGAGCAC GGCGTGCCCA
3551 TTCACGCCGA CAAGTACTTT GAGCAGGTTC TCAAGGCTGT AACTAACGTG
30 3601 CTGTCGCCC G TCTTTCCCG CGGCGAAACC GCGCGCAAGG ACAAGTTTTT
3651 GCACATGGTG CTGCCGCGGC GCTTGCACTT GGAGCCGGCT TTTCTGCCGT
3701 ACAGTGTC AA GGCGCACGAA TGCTGTTGA
35

SEQ. ID. NO. 12 Amino acid sequence of DNA polymerase for HCMV-AD169-M1

1 MFFNPYLSGG VTGGAVAGGR RQRSQPGSAQ GSGKRPPQKQ FLQIVPRGVM
 5 51 FDGQTGLIKH KTGRLLPLMFY REIKHLLSHD MVWPCPWRET LVGRVVGPIR
 101 FHTYDQTDV LFFDSPENV S PRYRQHLVPS GNVLRFFGAT EHGYSICVNV
 10 151 FGQRSYFYCE YSDTDRLREV IASVGELVPE PRTPYAVSVT PATKTSIYGY
 201 GTRPVPDLQC VSISNWTMAR KIGEYLLEQG FVVEYVRVDP LTRLVIDRRI
 251 TTFGWCSVNR YDWRQQGRAS TCDIEVDCDV SDLVAVPDDS SWPRYRCLSF
 15 301 DIECMSGEGG FPCAESDDI VIQISCVCYE TGGNTAVDQG IPNGNDGRGC
 351 TSEGVIHGHS GLHLFTIGTC GQVGPDVDVY EFPSEYELLL GFMLFFQRYA
 401 PAFVTGYNIN SFDLKYILTR LEYLYKVDSQ RFCKLPTAQG GRFFLHSPAV
 451 GFKRQYAAAF PSASHNNPAS TAATKVYIAG SVVIDMYPVC MAKTNSPNYK
 501 LNTMAELYLR QRKDDLSYKD IPRCFVANAE GRAQVGRYCL QDAVLVRDLF
 25 551 NTINFHYEAG AIARLAKIPL RRVIFDGQOI RIYTSLLDEC ACRDFILPNH
 601 YSKGTTVPET NSVAVSPNAA IISTAAVPGD AGSVAAMFQM SPPLQSAPSS
 30 651 QDGVSPGSGS NSSSSVGVFS VSGSGSSGGVG VSNDNHGAGG TAAVSYQGAT
 701 VFEPEVGYYN DPVAVDFAS LYPHIIMAHN LCYSTLLVPG GEYPVDPADV
 751 YSVTLENGVT HRFVVRASVRV SVLSELLNKW VSQRRVREC MRECQDPVRR
 35 801 MLLDKEQMAL KVTCAFYGF TGALNGMMPC LPIAASITRI GRDMLERTAR
 851 FIKDNFSEPC FLHNFFNQED YVVGTTREGDS EESSALPEGL ETSSGGSNER
 40 901 RVEARVTYGD TDSVFVRFRG LTPQALVARG PSLAHYVTAC LFVEPVKLEF
 951 EKVFSVSLMMI CKKRYIGKVE GASGLSMKGV DLVRKTACEF VKGVTRDVLS
 1001 LLFEDREVSE AAVRLSRLSL DEVKKYGVPR GFWRILRRLV QARDDLYLHR
 45 1051 VRVEDLVLS VLSKDISLYR QSNLPHIAVI KRLAARSEEL PSVGDRVFYV
 1101 LTAPGVRTAP QGSSDNGDSV TAGVVSRSDA IDGTDDDADG GGVEESNRRG
 1151 GEPAKKRARK PPSAVCNIEV AEDPSYVREH GVPIHADKYF EQVLKAVTNV
 50 1201 LSPVFPGET ARKDKFLHMLV LPRRLHLEPA FLPYSVKAHE CC*

55

Figure 6**SEQ.ID.NO.13****Amino acid sequence of DNA polymerase for HCMV-AD169**

5 1 MFFNPYLSGG VTGGAVAGGR RQRSQPGSAQ GSGKRPPQKQ FLQIVPRGVM
 51 FDGQTGLIKH KTGRLPLMFY REIKHLLSHD MVWPCPWRET LVGRVVGPIR
 101 FHTYDQTDV LFFDSPENV S PRYRQHLVPS GNVLRFFGAT EHGYSICVNV
 10 151 FGQRSYFYCE YSDTDRLREV IASVGELVPE PRTPYAVSVT PATKTSIYGY
 201 GTRPVLDLQC VSISNWTMAR KIGEYLLEQG FPVYEVRVDP LTRLVIDRRI
 251 TTFGWCSVNR YDWRQQGRAS TCDIEVDCDV SDLVAVPDDS SWPRYRCLSF
 15 301 DIECMSGEGG FPCAESDDI VIQISCVCYE TGGNTAVDQG IPNGNDGRGC
 351 TSEGVIHGHS GLHLFTIGTC GQVGPVDVY EFPSEYELLL GFMLFFQRYA
 20 401 PAFVTGYNIN SFDLKYILTR LEYLYKVDSQ RFCKLPTAQG GRFFLHSPAV
 451 GFKRQYAAAF PSASHNNPAS TAATKVYIAG SVVIDMYPVC MAKTNSPNYK
 501 LNTMAELYLR QRKDDLSYKD IPRCFVANAE GRAQVGRYCL QDAVLVRDLF
 25 551 NTINFHYEAG AIARLAKIPL RRVIFDGQOI RIYTSLLDEC ACRDFILPNH
 601 YSKGTTVPET NSVAVSPNAA IISTAAVPGD AGSVAAMFQM SPPLQSAPSS
 30 651 QDGVSPGSGS NSSSSVGVFS VSGSSSGGVG VSNDNHGAGG TAAVSYQGAT
 701 VFEPEVGYYN DPVAVDFDAS LYPSEIMAHN LCYSTLLVPG GEYPVDPADV
 751 YSVTLENGVT HRFVVRASVRV SVLSELLNKW VSQRRVREC MRECQDPVRR
 35 801 MLLDKEQMAL KVTCAFYGF TGVVNGMMPC LPIAASITRI GRDMLERTAR
 851 FIKDNFSEPC FLHNFFNQED YVVGTTREGDS EESSALPEGL ETSSGGSNER
 40 901 RVEARVIYGD TDSVFVRFRG LTPQALVARG PSLAHYVTAC LFVEPVKLEF
 951 EKVFSVSLMMI CKKRYIGKVE GASGLSMKGV DLVRKTACEF VKGVTRDVLS
 1001 LLFEDREVSE AAVRLSRLSL DEVKKYGVPR GFWRLRLRV QARDDLYLHR
 1051 VRVEDLVLS VLSKDISLYR QSNLPHIAVI KRLAARSEEL PSVGDRVFYV
 1101 LTAPGVRTAP QGSSDNGDSV TAGVVSRSDA IDGTDDDADG GGVEESNRRG
 50 1151 GEPAKKRARK PPSAVCNIEV AEDPSYVREH GVPIHADKYF EQVLKAVTNV
 1201 LSPVFPGET ARKDKFLHMLV LPRRLHLEPA FLPYSVKAHE CC*
 55